

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:05:18 ; Search time 38 Seconds  
(without alignments)  
1227.308 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836  
Sequence: 1 MSFYSKQDYNMDELDPEYNN.....GFLNNGIKADVLNHLCHM 350

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*  
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	100.0	350	22	AAE08003 Human chimeric NPY
2	1777	96.8	394	22	AAE08005 Human chimeric NPY
3	1777	96.8	394	23	ABR79512 Human chimeric NPY
4	1743	94.9	341	22	AAE08008 Chimeric neuropeptide
5	1699	92.5	341	22	AAE08014 Dog chimeric CNPY5
6	1693	92.1	383	22	AAE08009 Dog chimeric CNPY5
7	1691	92.1	352	22	AAE08011 Dog chimeric CNPY5
8	1668.5	90.9	455	17	AAE95939 Human Y5 receptor
9	1668.5	90.9	455	18	AAW29447 Human hippocampal
10	1668.5	90.9	455	18	AAW29413 Human hippocampal

11	1668.5	90.9	455	19	AAW37093 Homo sapiens hippo
12	1668.5	90.9	455	20	AAV57461 Human hippocampal
13	1668.5	90.9	455	22	AAE08002 Human neuropeptide
14	1668.5	90.9	455	23	ABR79510 Human neuropeptide
15	1665.5	90.7	455	22	AAE08016 African green monkey
16	1647	89.7	383	22	AAE08015 Pig chimeric CNPY5
17	1637	89.2	355	22	AAE08013 Rat chimeric CNPY5
18	1616.5	88.0	456	19	AAW37095 Canis domesticus Y
19	1613.5	87.9	445	18	AAW27604 Human neuropeptide
20	1613.5	87.9	445	18	AAW15230 Human neuropeptide
21	1613.5	87.9	445	20	AAV14554 Human neuropeptide
22	1613.5	87.9	445	21	AAV52578 Human NPY (neurope
23	1613.5	87.9	445	22	AAE07922 Human neuropeptide
24	1613.5	87.9	445	22	AAE07958 Human neuropeptide
25	1613.5	87.9	445	22	AAE06692 Human neuropeptide
26	1613.5	87.9	445	22	AAE85110 Human neuropeptide
27	1613.5	87.9	445	22	AAE85121 Human neuropeptide
28	1610.5	87.7	445	22	AAE02651 Rhesus neuropeptide
29	1609.5	87.7	499	22	AAE08004 Human chimeric NPY
30	1604.5	87.4	445	22	Non-endogenous hum
31	1549.5	84.4	445	21	AAV52577 Chimeric rat/human
32	1536	83.7	456	17	AAE95940 Rat Y5 receptor
33	1536	83.7	456	18	Rat hypothalamic n
34	1536	83.7	456	18	AAW29412 Rat hypothalamic n
35	1536	83.7	456	19	AAW37092 Rattus norvegicus
36	1536	83.7	456	20	AAV57460 Rat hypothalamic Y
37	1526	83.1	445	18	AAW27603 Rat neuropeptide Y
38	1526	83.1	445	20	AAV14553 Rat neuropeptide Y
39	1526	83.1	445	21	AAV52579 Rat NPY (neuropept
40	1524	83.0	445	18	AAW15232 Rat neuropeptide Y
41	1519	82.7	445	18	AAW27602 Rat neuropeptide Y
42	1519	82.7	445	20	AAV14552 Rat neuropeptide Y
43	1511.5	82.3	466	18	AAW15233 Mouse neuropeptide
44	1482	80.7	499	22	AAE08012 Rat chimeric CNPY5
45	1461.5	79.6	508	22	AAE08010 Mouse chimeric mmp

#### ALIGNMENTS

RESULT 1  
ID AAE08003 standard: Protein: 350 AA.  
XX AAE08003:  
AC  
XX  
DF 01-NOV-2001 (first entry)  
XX  
XX Human chimeric NPY5deltaY11C3 receptor.  
DE  
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
KW Transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;  
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;  
KW locomotor; anxiety disorder; limbic seizure; tranquilliser;  
KW human; chimeric receptor.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200155103-A2.  
PN  
XX  
XX 02-AUG-2001.  
PD  
XX  
XX 29-JAN-2001; 2001WO-US02804.  
PF  
XX  
XX 28-JAN-2000; 2000US-0178652.  
PR  
XX  
XX (NEUR-) NEUROGEN CORP.  
PA  
XX  
XX Bennett M, Brodbeck R, Krause J;  
PI  
XX  
XX WPI: 2001-514543/56.  
DR  
XX  
XX N-PSDB; AAD14735.



KM Neuropeptide Y; NPY; NPY5; NPY1; receptor; antagonist; anorectic;  
KM antinflammatory; nootropic; neuroprotective; cardiovascular;  
KM hypotensive; antidiabetic; psychiatric; anticonvulsant; caediant;  
KM cerebroprotective; antidepressant; haemostatic; tranquillizer;  
KM neuroleptic; analgesic; antianalgesic; nephrotropic; uropathic;  
KM gastrointestinal; antispasmodic; human; hnpysdeltayl1C3/deltayl1CT.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN MO200248152-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 11-DEC-2001; 2001MO-US47863.  
XX  
PR 12-DEC-2000; 2000US-254990P.  
XX  
PA (NEUR-) NEUROGEN CORP.  
XX  
PI Bakhtavatchalam R, Blum CA, Brielmann HL, Darrow JW, De Lombaert S;  
PI Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;  
XX  
DR WPI; 2002-547845/58.  
DR N-PSDB; ABN84260.  
XX  
PT New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or  
PT 3H-spiro(isobenzofuran-1,4'-piperidine) useful for treating, e.g. eating  
PT disorder, psychiatric, cardiovascular disorder or diabetes -  
XX  
XX Example 675; Page 134; 134pp; English.  
XX  
CC The present sequence is the protein sequence for chimeric human  
CC neuropeptide receptor hnpysdeltayl1C3/deltayl1CT, stated to comprise  
CC the N-terminal amino acids 1-442 of the human neuropeptide Y5 (NPY5)  
CC receptor and the C-terminal amino acids 328-384 of the human NPY1  
CC receptor. The recombinant chimeric receptor was produced in Sf9  
CC cells using a baculovirus expression vector. It was used to assay  
CC the binding activity of compounds of the invention. Substituted  
CC spiro(isobenzofuran-1,4'-piperidin)-3-ones and  
CC 3H-spiro(isobenzofuran-1,4'-piperidines) capable of modulating NPY5  
CC receptor activity are provided. Such compounds may be used to  
CC modulate ligand binding to NPY5 receptors in vivo or in vitro,  
CC and are particularly useful in the treatment of a variety of  
CC disorders, e.g. eating disorders such as obesity or bulimia,  
CC psychiatric disorders, diabetes and cardiovascular disorders such  
CC as hypertension, in humans and animals.  
XX  
XX  
SQ Sequence 394 AA:  
XX  
Query Match 96.8%; Score 1777; DB 23; Length 394;  
Best Local Similarity 99.4%; Pred. No. 1.4e-181;  
Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 MSFYSKODYNMDELDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTF 60  
Db 1 MSFYSKODYNMDELDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTF 60  
XX  
QY 61 VSLGFGNGLIIMALKRNRKQTVNFIIGNAFSDILVYLFCSPTLTSLVLDQMFG 120  
Db 61 VSLGFGNGLIIMALKRNRKQTVNFIIGNAFSDILVYLFCSPTLTSLVLDQMFG 120  
XX  
QY 121 KWCHIMPFLOCYSLVSTLILISIAIVRYHMTKHPISNNLTANHGFLATYWTGLFAI 180  
Db 121 KWCHIMPFLOCYSLVSTLILISIAIVRYHMTKHPISNNLTANHGFLATYWTGLFAI 180  
XX  
QY 181 CSPLPVFHSLSVLEQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYTLPLVCLTVS 240  
Db 181 CSPLPVFHSLSVLEQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYTLPLVCLTVS 240  
XX  
QY 241 HTSVCIIRLKRNRNMMDKRNKRSSRSRSVFRKTLTLLIVFAVSMPPLHFFHVTFDND 300  
Db 241 HTSVCIIRLKRNRNMMDKRNKRSSRSRSVFRKTLTLLIVFAVSMPPLHFFHVTFDND 300

QY 301 NLISNRHFKLTYCICHLGMMSCCLNPILYGLNNGIKADL 341  
Db 301 NLISNRHFKLTYCICHLGMMSCCLNPILYGLNNGIKADL 341  
XX  
RESULT 4  
AAE08008  
ID AAE08008 standard; Protein; 341 AA.  
XX  
AC AAE08008;  
XX  
DT 01-NOV-2001 (first entry)  
XX  
DE Dog chimeric CNPY5deltayl1C3 receptor.  
XX  
KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;  
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;  
KW locomotor; anxiety disorder; limbic seizure; tranquilliser;  
KW dog; chimeric receptor.  
XX  
OS Canis sp.  
XX  
PN WO200155103-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001MO-US02804.  
XX  
PR 28-JAN-2000; 2000US-0178652.  
XX  
PA (NEUR-) NEUROGEN CORP.  
XX  
PI Bennett M, Brodbeck R, Krause J;  
XX  
DR WPI; 2001-514543/56.  
XX  
PT New chimeric receptor proteins comprising a single polypeptide chain of  
PT amino acids, useful as targets for drug actions, and as basis for drug  
PT discovery and development -  
XX  
XX Example 2; Page 58-59; 72pp; English.  
XX  
CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.  
CC The NPY receptors are G-protein-coupled transmembrane proteins with  
CC seven membrane spanning transmembrane (TM) domains. The compounds that  
CC modulate the activity of a NPY receptor is useful in the preparation of  
CC a medicament for treating conditions including obesity, high/low blood  
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,  
CC seizure, locomotor and anxiety disorders. They can also be used as  
CC targets for drug actions, and as basis for drug discovery and  
CC development. The NPY5 receptor may have an anti-epileptic activity in  
CC the control of limbic seizures. The present sequence is dog chimeric  
CC CNPY5deltayl1C3 receptor. The chimera comprises intracellular  
CC loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1  
CC receptor.  
XX  
XX  
SQ Sequence 341 AA:  
XX  
Query Match 94.9%; Score 1743; DB 22; Length 341;  
Best Local Similarity 97.6%; Pred. No. 5.2e-178;  
Matches 332; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 11 MDELDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTVSLLGFGNLT 70  
Db 11 MDELDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTVSLLGFGNLT 70  
XX  
QY 71 LILMALKRNRKQTVNFIIGNAFSDILVYLFCSPTLTSLVLDQMFGKVMCHIMPFL 130  
Db 71 LILMALKRNRKQTVNFIIGNAFSDILVYLFCSPTLTSLVLDQMFGKVMCHIMPFL 130  
XX  
QY 131 QCVSVLSTLILISIAIVRYHMTKHPISNNLTANHGFLATYWTGLFAICSPLPVHSL 190  
Db 131 QCVSVLSTLILISIAIVRYHMTKHPISNNLTANHGFLATYWTGLFAICSPLPVHSL 190

```

Db 121 QCVSYLSTLLISLAIRYMIKHPISNNLTANHGYFLITVMTLGFALCSPLVPHSL 180
QY 191 VELOEFGSALLSRYLCVESMPSPDSYRIAFITISLLVQYILPLVCLTVSHTSVCIRLKR 250
Db 181 VELOEFGSALLSRYLCVESMPSPDSYRIAFITISLLVQYILPLVCLTVSHTSVCIRLKR 240
QY 251 RNNMMDKMRDNKRYSSRSRSVFYRLTILILVFAVSWMPHLHFVYVTFDNDMLISNRHEKL 310
Db 241 RNNMMDKMRDNKRYSSRSRSVFYRLTILILVFAVSWMPHLHFVYVTFDNDMLISNRHEKL 300
QY 311 VYCICHLLGMSSCCLPILYGFLLNGIKADLVSLIHCHLM 350
Db 301 VYCICHLLGMSSCCLPILYGFLLNGIKADLVSLIHCHLM 340

RESULT 5
AAE08014
ID AAE08014 standard; Protein: 341 AA.
AC AAE08014;
DT 01-NOV-2001 (first entry)
XX
XX Pig chimeric pNPY5deltapyl1C3 receptor.
DE
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
XX transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
XX Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
XX locomotor; anxiety disorder; limbic seizure; tranquilliser;
XX pig; chimeric receptor.
XX
XX Cavia sp.
OS
XX WO200155103-A2.
XX
XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US02804.
XX
XX 28-JAN-2000; 2000US-0178652.
XX
XX (NEUR-) NEUROGEN CORP.
PA
XX Bennett M, Brodbeck R, Krause J;
XX
XX WPI; 2001-514543/56.
XX
XX New chimeric receptor proteins comprising a single polypeptide chain of
XX amino acids, useful as targets for drug actions, and as basis for drug
XX discovery and development -
XX
XX Example 2; Page 67-68; 72pp; English.
XX
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
XX The NPY receptors are G-protein-coupled transmembrane proteins with
XX seven membrane spanning transmembrane (TM) domains. The compounds that
XX modulate the activity of a NPY receptor is useful in the preparation of
XX a medicament for treating conditions including obesity, high/low blood
XX pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
XX seizure, locomotor and anxiety disorders. They can also be used as
XX targets for drug actions, and as basis for drug discovery and
XX development. The NPY5 receptor may have an anti-epileptic activity in
XX the control of limbic seizures. The present sequence is pig chimeric
XX pNPY5deltapyl1C3 receptor. The chimera comprises intracellular
XX loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1
XX receptor.
XX
XX Sequence 341 AA;
SQ

```

```

QY 11 MDLEIDEXYNTLATENNNTAATRNSPDFWDDYKSSVDLDQYFLIGLYTFVSLGFMGNL 70
Db 1 MGSEIPDYNNKTLASENTVATRNNGCFPWMEDEYKGSVDLDQYFLIGLYTFVSLGFMGNL 60
QY 71 LILAAAMKRRQKTTVNFILGNLAFSDLLVLFCSPFLLTSVLLDDQWFGVKCHIMEFL 130
Db 61 LILAAVMRRKQKTTVNFILGNLAFSDLLVLFCSPFLLTSVLLDDQWFGVKCHIMEFL 120
QY 131 QCVSYLSTLLISLAIRYMIKHPISNNLTANHGYFLITVMTLGFALCSPLVPHSL 190
Db 121 QCVSYLSTLLISLAIRYMIKHPISNNLTANHGYFLITVMTLGFALCSPLVPHSL 180
QY 191 VELOEFGSALLSRYLCVESMPSPDSYRIAFITISLLVQYILPLVCLTVSHTSVCIRLKR 250
Db 181 VELOEFGSALLSRYLCVESMPSPDSYRIAFITISLLVQYILPLVCLTVSHTSVCIRLKR 240
QY 251 RNNMMDKMRDNKRYSSRSRSVFYRLTILILVFAVSWMPHLHFVYVTFDNDMLISNRHEKL 310
Db 241 RNNMMDKMRDNKRYSSRSRSVFYRLTILILVFAVSWMPHLHFVYVTFDNDMLISNRHEKL 300
QY 311 VYCICHLLGMSSCCLPILYGFLLNGIKADLVSLIHCHLM 350
Db 301 VYCICHLLGMSSCCLPILYGFLLNGIKADLVSLIHCHLM 340

RESULT 6
AAE08009
ID AAE08009 standard; Protein: 383 AA.
AC AAE08009;
DT 01-NOV-2001 (first entry)
XX
XX Dog chimeric cNPY5deltapyl1C3/deltapyl1C1 receptor.
DE
XX
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
XX transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
XX Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
XX locomotor; anxiety disorder; limbic seizure; tranquilliser;
XX dog; chimeric receptor.
XX
XX Canis sp.
OS
XX WO200155103-A2.
XX
XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US02804.
XX
XX 28-JAN-2000; 2000US-0178652.
XX
XX (NEUR-) NEUROGEN CORP.
PA
XX Bennett M, Brodbeck R, Krause J;
XX
XX WPI; 2001-514543/56.
XX
XX New chimeric receptor proteins comprising a single polypeptide chain of
XX amino acids, useful as targets for drug actions, and as basis for drug
XX discovery and development -
XX
XX Example 2; Page 59-60; 72pp; English.
XX
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
XX The NPY receptors are G-protein-coupled transmembrane proteins with
XX seven membrane spanning transmembrane (TM) domains. The compounds that
XX modulate the activity of a NPY receptor is useful in the preparation of
XX a medicament for treating conditions including obesity, high/low blood
XX pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
XX seizure, locomotor and anxiety disorders. They can also be used as
XX targets for drug actions, and as basis for drug discovery and
XX development. The NPY5 receptor may have an anti-epileptic activity in
XX

```

CC the control of limbic seizures. The present sequence is a dog chimeric  
CC cnpysdeltar11c3/deltar1c1 receptor. The chimera comprises  
CC intracellular loop 3 and C-terminal intracellular domain of NPY5 receptor  
CC replaced with intracellular loop 3 and C-terminal intracellular domain  
CC respectively, of NPY1 receptor.

XX  
SQ Sequence 383 AA:

Query Match 92.2%; Score 1693; DB 22; Length 383;

Best Local Similarity 97.6%; Pred. No. 1.4e-172;

Matches 323; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 MDLELDYVTKTLATENNATRNSDFPVWDYKSSVDLQYFLGLGYFVSLGFMGNL 70

DB 1 MDLELDYVTKTLATENNATRNSDFPVWDYKSSVDLQYFLGLGYFVSLGFMGNL 60

QY 71 LILMALMKRNOKTYVNFLLGNLAFSDIIVLVLCSPFTLTVSLLDDMFCKVCHIMPEL 130

DB 61 LILMALMKRNOKTYVNFLLGNLAFSDIIVLVLCSPFTLTVSLLDDMFCKVCHIMPEL 120

QY 131 QCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPVPHSL 190

DB 121 QCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPVPHSL 180

QY 191 VELQETFGSALLSRYLCVESMPDSSTYRIAFITSLILVOYILPLVCLTVSHTSVCIRLKR 230

DB 181 VELQETFGSALLSRYLCVESMPDSSTYRIAFITSLILVOYILPLVCLTVSHTSVCIRLKR 240

QY 251 RNNMMKMRNKRKSSRSRSRVFRLTILLVFAVSMPLHPLFVYVDFNDNLISNRHFKL 310

DB 241 RNNMMKMRNKRKSSRSRSRVFRLTILLVFAVSMPLHPLFVYVDFNDNLISNRHFKL 300

QY 311 VVCICHLGMMSCCLNPILYGFLLNGIKADL 341

DB 301 VVCICHLGMMSCCLNPILYGFLLNGIKADL 331

RESULT 7

AAE08011 standard; Protein; 352 AA.

AC AAE08011;

DT 01-NOV-2001 (first entry)

DE Rat chimeric rnpysdeltar1c3 receptor.

KM Neuropeptide Y, NPY receptor; G-protein-coupled transmembrane protein;

KM Transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;

KM Huntington's disorder; Parkinson's disorder; eating disorder; seizure;

KM locomotor; anxiety disorder; limbic seizure; tranquilliser;

XX rat; chimeric receptor.

OS Rattus sp.

PN WO200155103-A2.

PD 02-AUG-2001.

PF 29-JAN-2001; 2001WO-US02804.

PR 28-JAN-2000; 2000US-0178652.

PA (NEUR-) NEUROGEN CORP.

PI Bennett M, Brodbeck R, Krause J;

DR WPI; 2001-514543/56.

XX New chimeric receptor proteins comprising a single polypeptide chain of  
PT amino acids, useful as targets for drug actions, and as basis for drug  
PT discovery and development -  
XX

PS Example 2; Page 62-63; 72pp; English.

XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.

CC The NPY receptors are G-protein-coupled transmembrane proteins with

CC seven membrane spanning transmembrane (TM) domains. The compounds that

CC modulate the activity of a NPY receptor is useful in the preparation of

CC a medicament for treating conditions including obesity, high/low blood

CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,

CC seizure, locomotor and anxiety disorders. They can also be used as

CC targets for drug actions, and as basis for drug discovery and

CC development. The NPY5 receptor may have an anti-epileptic activity in

CC the control of limbic seizures. The present sequence is rat chimeric

CC rnpysdeltar11c3 receptor. The chimera comprises intracellular

CC loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1

XX receptor.

SQ Sequence 352 AA:

Query Match 92.1%; Score 1691; DB 22; Length 352;

Best Local Similarity 92.4%; Pred. No. 2e-172;

Matches 318; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 7 QDYNMDELDYVTKTLATENNATRNSDFPVWDYKSSVDLQYFLGLGYFVSLGFMGNL 66

DB 8 QDSSMEFKLEHFNKTFVTEENNTAAARNAPAMEDYRGSDVDLQYFLGLGYFVSLGFMGNL 67

QY 67 MGNLILMALMKRNOKTYVNFLLGNLAFSDIIVLVLCSPFTLTVSLLDDMFCKVCHIMPEL 126

DB 68 MGNLILMALMKRNOKTYVNFLLGNLAFSDIIVLVLCSPFTLTVSLLDDMFCKVCHIMPEL 127

QY 127 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPV 186

DB 128 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPV 187

QY 187 FHSVLVELOEFGSALLSRYLCVESMPDSSTYRIAFITSLILVOYILPLVCLTVSHTSVCI 246

DB 188 FHSVLVELOEFGSALLSRYLCVESMPDSSTYRIAFITSLILVOYILPLVCLTVSHTSVCI 247

QY 247 RLKRRNNMMDKMRNKRKSSRSRSRVFRLTILLVFAVSMPLHPLFVYVDFNDNLISNR 306

DB 248 RLKRRNNMMDKMRNKRKSSRSRSRVFRLTILLVFAVSMPLHPLFVYVDFNDNLISNR 307

QY 307 HFKLVYICICHLGMMSCCLNPILYGFLLNGIKADLVSILHCLHM 350

DB 308 HFKLVYICICHLGMMSCCLNPILYGFLLNGIKADLVSILHCLHM 351

RESULT 8

AAR95939 standard; Protein; 455 AA.

AC AAR95939;

DT 14-OCT-1996 (first entry)

DE Human Y5 receptor.

KM Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior;

KM G protein-coupled receptor; agonist; antagonist; obesity;

XX bulimia; anorexia; transgenic animal.

OS Homo sapiens.

PN Key

FT Location/Qualifiers

FT 51..77

FT /label= I

FT /note= "Transmembrane domain I"

FT 88..110

FT /label= II

FT /note= "Transmembrane domain II"

FT 126..147

FT /label= III

FT /note= "Transmembrane domain III"

```
FT  Domain 166..187
FT  /label= IV
FT  /note= "transmembrane domain IV"
FT  Domain 220..242
FT  /label= V
FT  /note= "transmembrane domain V"
FT  Domain 380..403
FT  /label= VI
FT  /note= "transmembrane domain VI"
FT  Domain 416..438
FT  /label= VII
FT  /note= "transmembrane domain VII"
XX  M09616542-A1.
XX  06-JUN-1996.
XX  01-DEC-1995; 95MO-US15646.
XX  02-DEC-1994; 94US-0349025.
XX  (SYNA-) SYNAPTIC PHARM CORP.
XX  Branchek T, Gerald CPG, Walker MM, Weinschank RL;
XX  WPI; 1996-277371/28.
XX  N-PSDB; AAT30433.
XX  Modifying feeding behaviour using Y5 receptor (ant)agonists -
XX  increases or decreases food consumption, for treatment of e.g.
XX  obesity or bulimia
XX  Claim 51; Fig 6; 235pp; English.
XX  Human hippocampal Y5 receptor (AAR95939) was identified as the
XX  homologue of rat hypothalamic Y5 receptor (AAR95940), isolated
XX  as an 'atypical Y1 receptor'. The receptor belongs to the G
XX  protein-coupled receptor superfamily. It is encoded by a cDNA
XX  clone (see also AAT30433) that was isolated from a hippocampus cDNA
XX  library using rat Y5 receptor cDNA as probe. Recombinant rat Y5
XX  receptor can be produced in prokaryotic or eukaryotic (e.g. COS,
XX  293 or Sf9 insect) host cells. It is used to identify Y5 ligands
XX  (agonists and antagonists) that can be used to treat obesity,
XX  bulimia or anorexia, and to raise monoclonal antibodies useful in
XX  detecting Y5 receptor.
XX  Sequence 455 AA;
XX  SQ
XX  Query Match 90.9%; Score 1668.5; DB 17; Length 455;
XX  Best Local Similarity 73.2%; Pred. No. 7.3e-170;
XX  Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
```

```
Db 301 KKTACVLPAPERPSQENSRILPENFGSVRSQSSSKFIPGVPTCEIKPENSDVHEL 360
Oy 265 -----SSRSRSVFRLITLLVFVAVSWMPHLFHVVDNDNLISNHFPLVYIC 315
Db 361 RYKRSVTRIKKRSKSVFRLITLLVFVAVSWMPHLFHVVDNDNLISNHFPLVYIC 420
Oy 316 HLLGMSCCLNPILYGFLLNGIRKADLVSLINCLHM 350
Db 421 HLLGMSCCLNPILYGFLLNGIRKADLVSLINCLHM 455
XX  RESULT 9
XX  AAW29447
XX  ID AAW29447 standard; Protein: 455 AA.
XX  AC AAW29447;
XX  XX 26-FEB-1998 (first entry)
XX  DE Human hippocampal neuropeptide Y Y5 receptor.
XX  KW Hippocampal; neuropeptide Y Y5 receptor; NPY Y5; antagonist;
XX  KW epileptic seizure; migraine; sleep disturbance; propylaxis;
XX  KW eating disorder; quinzolin-2,4-diazirine.
XX  OS Homo sapiens.
XX  PN W09720822-A1.
XX  PD 12-JUN-1997.
XX  PF 18-NOV-1996; 96MO-EP05066.
XX  PR 01-DEC-1995; 95US-0566027.
XX  PA (NOVS ) NOVARTIS AG.
XX  PI Criscione L, Rigollier P, Rueger H, Schilling W;
XX  PI Schmidlin T, Tintelnnot-blomley M, Yamaguchi Y;
XX  PI Tintelnnot-blomley M;
XX  DR WPI; 1997-319712/29.
XX  N-PSDB; AAT89114.
XX  Use of new and known quinzolin-2,4-diazirine compounds as NPY Y5
XX  receptor antagonists - for treating and preventing eating disorders,
XX  diabetes, dyslipidaemia, hypertension, memory loss, epileptic
XX  seizures, migraine, sleep disturbance, etc
XX  PS Disclosure; Pages 127-129; 155pp; English.
XX  CC The present sequence represents human hippocampal neuropeptide
XX  CC (NP) Y receptor subtype Y5, with a pharmacological function associated
XX  CC with for example, obesity and eating disorders. The specification relates
XX  CC to a method of treatment and prophylaxis of disorders and diseases
XX  CC associated with with NPY receptor subtype Y5 comprising administering to
XX  CC a warm-blooded animal, including man, in need of such treatment a
XX  CC therapeutically effective amount of a quinzolin-2,4-diazirine
XX  CC compound. These disorders and diseases include e.g. eating disorders,
XX  CC obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory
XX  CC loss, epileptic seizures, migraine, sleep disturbance, pain,
XX  CC sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage,
XX  CC shock, congestive heart failure, nasal congestion or diarrhoea.
XX  SQ Sequence 455 AA;
XX  Query Match 90.9%; Score 1668.5; DB 18; Length 455;
XX  Best Local Similarity 73.2%; Pred. No. 7.3e-170;
XX  Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
```

```
Db 1 MSFYSKODYNMDELDEYYNKTATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
QY 61 VSLGFGNLLIIMALKKRNOKTTFVNLGNLAFSDILVLFCSPTLTSLVLDQMFG 120
Db 61 VSLGFGNLLIIMALKKRNOKTTFVNLGNLAFSDILVLFCSPTLTSLVLDQMFG 120
QY 121 KVMCHIMPFLOQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLIATWTGFAI 180
Db 121 KVMCHIMPFLOQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLIATWTGFAI 180
QY 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITSLILVOYILPLVCLTVS 240
Db 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITSLILVOYILPLVCLTVS 240
QY 241 HTSVC-----IRLKRNNMMK----- 257
Db 241 HTSVCISGCLSNKRELBENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300
QY 258 -----MRDKYR----- 264
Db 301 KKTACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDHEL 360
QY 265 -----SSRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYYCIC 315
Db 361 RVRKSVTRIKRRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYYCIC 420
QY 316 HLLGMMSCCLPILYGFLLNGIKADLVSLIHCLHM 350
Db 421 HLLGMMSCCLPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 10
AAM29413
ID AAM29413 standard; Protein; 455 AA.
XX
AC AAM29413;
XX
DT 24-FEB-1998 (first entry)
XX
DE Human hippocampal neuropeptide Y Y5 receptor.
XX
KW Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis;
KW bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss;
KW epileptic seizure; migraine; sleep disturbance; pain; depression;
KW sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea;
KW congestive heart failure; eating disorder; obesity.
XX
OS Homo sapiens.
XX
PN MO9720820-A1.
XX
PD 12-JUN-1997.
XX
PF 18-NOV-1996; 96MO-EP05055.
XX
PR 01-DEC-1995; 95US-0566349.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Crisstone L, Rigollier P, Rueger H, Schilling W;
PI Schmidlin T, Tintelnot-Biomley M, Yamaguchi Y;
DR WPI; 1997-319711/29.
XX
N-PSDB; AAT89110.
XX
PT use of new and known heteroaryl compounds as NPY Y5-receptor
PT antagonists - for treating and preventing eating disorders,
PT diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
PT migraine, etc.
XX
PS Disclosure; Pages 76-78; 155pp; English.
XX
CC This sequence represents human hippocampal neuropeptide (NP) Y receptor
```

```
CC subtype Y5, with a pharmacological function associated with for example,
CC obesity and eating disorders. The specification relates to a method of
CC treatment and prophylaxis of disorders and diseases associated with
CC NPY receptor subtype Y5 comprising administering to a warm-blooded
CC animal, including man, in need of such treatment a therapeutically
CC effective amount of a new heteroaryl compound. These disorders and
CC diseases include e.g. eating disorders, obesity, bulimia nervosa,
CC diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
CC migraine, sleep disturbance, pain, sexual/reproductive disorders,
CC depression, anxiety, cerebral haemorrhage, shock, congestive heart
CC failure, nasal congestion or diarrhoea.
XX
SQ Sequence 455 AA:
XX
Query Match 90.9%; Score 1668.5; DB 18; Length 455;
Best Local Similarity 73.2%; Pred. No. 7.3e-170;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 1 MSFYSKODYNMDELDEYYNKTATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
Db 1 MSFYSKODYNMDELDEYYNKTATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
QY 61 VSLGFGNLLIIMALKKRNOKTTFVNLGNLAFSDILVLFCSPTLTSLVLDQMFG 120
Db 61 VSLGFGNLLIIMALKKRNOKTTFVNLGNLAFSDILVLFCSPTLTSLVLDQMFG 120
QY 121 KVMCHIMPFLOQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLIATWTGFAI 180
Db 121 KVMCHIMPFLOQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLIATWTGFAI 180
QY 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITSLILVOYILPLVCLTVS 240
Db 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITSLILVOYILPLVCLTVS 240
QY 241 HTSVC-----IRLKRNNMMK----- 257
Db 241 HTSVCISGCLSNKRELBENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300
QY 258 -----MRDKYR----- 264
Db 301 KKTACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDHEL 360
QY 265 -----SSRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYYCIC 315
Db 361 RVRKSVTRIKRRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYYCIC 420
QY 316 HLLGMMSCCLPILYGFLLNGIKADLVSLIHCLHM 350
Db 421 HLLGMMSCCLPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 11
AAM37093
ID AAM37093 standard; Protein; 455 AA.
XX
AC AAM37093;
XX
DT 08-JUN-1998 (first entry)
XX
DE Homo sapiens hippocampal Y5 receptor.
XX
KW Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity;
KW feeding behaviour; modification; atypical neuropeptide.
XX
OS Homo sapiens.
XX
PN MO9746250-A1.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97MO-US09504.
XX
PR 21-FEB-1997; 97US-0803600.
```

PR 04-JUN-1996; 96US-0668650.  
XX  
PA (SYNA-) SYNAPTIC PHARM CORP.  
XX  
PI Branchek T, Gerald CP, Walker MW, Weinschank RL;  
XX  
DR WPI: 1998-051901/05.  
DR N-PSDB; AAV00622.  
XX  
PT DNA encoding canine hypothalamic atypical neuro-peptide Y-peptide Y  
PT receptor, Y5 - useful for identification of compounds which are  
PT capable of modifying feeding behaviour  
XX  
PS Disclosure; Fig 6; 273pp; English.  
XX  
CC The sequence is that of a hippocampal Y5 receptor (Y5-R).  
CC Y5-r can be used in processes to determine whether a chemical compound  
CC specifically binds to and activates or inhibits a Y5-R by measuring a  
CC second messenger response. The chemical compounds can be used to  
CC increase or reduce the activity of a Y5-R. In particular, inhibitors  
CC can be used to treat obesity and activators can be used to treat  
CC anorexia. Antagonists capable of alleviating (by decreasing the  
CC activity of Y5-R) an abnormality can be identified by administering a  
CC potential antagonist to a transgenic mammal as above, and determining  
CC whether the substance alleviates the physical and behavioural  
CC abnormalities displayed by the transgenic mammal as a result of  
CC overactivity of a Y5-R. Agonists can be identified in a similar manner,  
CC but where the abnormality is alleviated by increasing the activity of  
CC Y5-R.  
XX  
XX Sequence 455 AA;  
SO  
Query Match 90.9%; Score 1668.5; DB 19; Length 455;  
Best Local Similarity 73.2%; Pred. No. 7.3e-170;  
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 1 MSFYSKODYNMDLEDEYKNTLATENTATRNSDPVPMDYKSSVDDLOFLIGLYTF 60  
DB 1 MSFYSKODYNMDLEDEYKNTLATENTATRNSDPVPMDYKSSVDDLOFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALKKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120  
DB 61 VSLGFMGNLLILMALKKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120  
QY 121 KVMCHIMPLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGFLLATWTGFAI 180  
DB 121 KVMCHIMPLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGFLLATWTGFAI 180  
QY 121 KVMCHIMPLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGFLLATWTGFAI 180  
DB 121 KVMCHIMPLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGFLLATWTGFAI 180  
QY 181 CSPLPVHSLVELOETFGSALLSRYLCEVSPDSYRIAFITISLLVOYITLPLVCLTVS 240  
DB 181 CSPLPVHSLVELOETFGSALLSRYLCEVSPDSYRIAFITISLLVOYITLPLVCLTVS 240  
QY 241 HTSVCSISGLSNKRELEENIMINTLHPSKKSQPVKLSGSHKMSYSFIKKHRRYS 300  
DB 241 HTSVCSISGLSNKRELEENIMINTLHPSKKSQPVKLSGSHKMSYSFIKKHRRYS 300  
QY 258 -----MRDNKYR----- 264  
DB 301 KKTACVLPAPERPSQEHNSRILPENFGSVRSQSSSKFTPGVPTCEFIKPEENSVDHEL 360  
QY 265 -----SSRSRVYRYLTLILVFAVSMPLHLFHYVVDNFNDNISNHFLLVYCIC 315  
DB 361 RVRKRSVTRIKRSRSVYRYLTLILVFAVSMPLHLFHYVVDNFNDNISNHFLLVYCIC 420  
QY 316 HLGMMSCCLNPLILGYFLNNGIKADLVSLIHCLHM 350  
DB 421 HLGMMSCCLNPLILGYFLNNGIKADLVSLIHCLHM 455  
RESULT 12  
AAV57461  
ID AAV57461 standard; Protein; 455 AA.  
XX

AC AAV57461;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Human hippocampal Y5 receptor.  
XX  
XX Y5 receptor; feeding behaviour; food consumption; obesity; bulimia;  
KW anorexia; neuropeptide; genetic engineering.  
XX  
OS Homo sapiens.  
XX  
PN US968819-A.  
XX  
PD 19-OCT-1999.  
XX  
PF 01-DEC-1995; 95US-0566096.  
XX  
PR 02-DEC-1994; 94US-0349025.  
XX  
PA (SYNA-) SYNAPTIC PHARM CORP.  
XX  
PI Walker MW, Branchek T, Gerald CP, Weinschank RL;  
XX  
DR WPI: 1999-590415/50.  
DR N-PSDB; AAZ39046.  
XX  
PT Nucleic acid encoding a human neuropeptide Y receptor useful in genetic  
PT engineering -  
XX  
PS Disclosure; Fig 6; 87pp; English.  
XX  
CC The present sequence represents the human hippocampal Y5 receptor. The Y5  
CC receptor is a G-protein coupled neuropeptide Y receptor found throughout  
CC the mammalian nervous system and is a powerful stimulant of feeding  
CC behaviour. Cells expressing DNA encoding the Y5 receptor can be used to  
CC determine whether a ligand specifically binds to a Y5 receptor. These  
CC cells or a cell extract, is exposed to the ligand and then any binding  
CC between the ligand and the receptor can be detected. The cells can also  
CC be used to determine whether a ligand is a Y5 receptor antagonist or  
CC agonist. The binding of chemical compounds to a Y5 receptor can also  
CC be determined and whether they activate or inhibit the activation of the  
CC Y5 receptor can also be determined using cells expressing the receptor.  
CC The effect of drugs on the Y5 receptor and whether they act as agonists  
CC or antagonists can also be detected with these cells.  
XX  
XX Sequence 455 AA;  
SO  
Query Match 90.9%; Score 1668.5; DB 20; Length 455;  
Best Local Similarity 73.2%; Pred. No. 7.3e-170;  
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 1 MSFYSKODYNMDLEDEYKNTLATENTATRNSDPVPMDYKSSVDDLOFLIGLYTF 60  
DB 1 MSFYSKODYNMDLEDEYKNTLATENTATRNSDPVPMDYKSSVDDLOFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALKKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120  
DB 61 VSLGFMGNLLILMALKKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120  
QY 121 KVMCHIMPLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGFLLATWTGFAI 180  
DB 121 KVMCHIMPLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGFLLATWTGFAI 180  
QY 181 CSPLPVHSLVELOETFGSALLSRYLCEVSPDSYRIAFITISLLVOYITLPLVCLTVS 240  
DB 181 CSPLPVHSLVELOETFGSALLSRYLCEVSPDSYRIAFITISLLVOYITLPLVCLTVS 240  
QY 241 HTSVCSISGLSNKRELEENIMINTLHPSKKSQPVKLSGSHKMSYSFIKKHRRYS 300  
DB 241 HTSVCSISGLSNKRELEENIMINTLHPSKKSQPVKLSGSHKMSYSFIKKHRRYS 300  
QY 258 -----MRDNKYR----- 264  
DB 301 KKTACVLPAPERPSQEHNSRILPENFGSVRSQSSSKFTPGVPTCEFIKPEENSVDHEL 360  
QY 265 -----SSRSRVYRYLTLILVFAVSMPLHLFHYVVDNFNDNISNHFLLVYCIC 315  
DB 361 RVRKRSVTRIKRSRSVYRYLTLILVFAVSMPLHLFHYVVDNFNDNISNHFLLVYCIC 420  
QY 316 HLGMMSCCLNPLILGYFLNNGIKADLVSLIHCLHM 350  
DB 421 HLGMMSCCLNPLILGYFLNNGIKADLVSLIHCLHM 455  
RESULT 12  
AAV57461  
ID AAV57461 standard; Protein; 455 AA.  
XX



Db 301 KKTACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIPGVPCTCEIKPEENSDVHEL 360  
QY 265 -----SSRSRSVFRYLITILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 315  
Db 361 RVRKSVTRIKRSRSVFRYLITILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
QY 316 HLLGMSSCCLNPILYGLFNGIKADLVSLIHCLHM 350  
Db 421 HLLGMSSCCLNPILYGLFNGIKADLVSLIHCLHM 455  
RESULT 13  
AAE08002  
ID AAE08002 standard; Protein; 455 AA.  
AC AAE08002;  
XX  
XX  
DT 01-NOV-2001 (first entry)  
XX  
DE Human neuropeptide Y5 (NPY5) receptor.  
XX  
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
KM transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;  
KM Huntington's disorder; Parkinson's disorder; eating disorder; seizure;  
KM locomotor; anxiety disorder; limbic seizure; tranquilliser; human.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Domain 1..50  
FT Domain /note= "N-terminal extracellular domain"  
FT Domain 51..71  
FT Domain /note= "First TM domain"  
FT Domain 72..84  
FT Domain /note= "First intracellular loop domain"  
FT Domain 85..105  
FT Domain /note= "Second TM domain"  
FT Domain 106..125  
FT Domain /note= "First extracellular loop domain"  
FT Domain 126..146  
FT Domain /note= "Third TM domain"  
FT Domain 147..167  
FT Domain /note= "Second intracellular loop domain"  
FT Domain 168..188  
FT Domain /note= "Fourth TM domain"  
FT Domain 189..220  
FT Domain /note= "Second extracellular loop domain"  
FT Domain 221..241  
FT Domain /note= "Fifth TM domain"  
FT Domain 242..378  
FT Domain /note= "Third intracellular loop domain"  
FT Domain 379..401  
FT Domain /note= "Sixth TM domain"  
FT Domain 402..414  
FT Domain /note= "Third extracellular loop domain"  
FT Domain 415..438  
FT Domain /note= "Seventh TM domain"  
FT Domain 439..455  
FT Domain /note= "C-terminal intracellular domain"  
XX  
PN W020015103-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 29-JAN-2001; 2001WO-US02804.  
XX  
XX 28-JAN-2000; 2000US-0178652.  
XX  
XX (NEUR-) NEUROGEN CORP.  
XX  
XX PA Bennett M, Brodbeck R, Krause J;  
XX PI  
XX WPI; 2001-514543/56.  
DR

DR N-PSDB; AAD14734.  
XX  
XX  
PT New chimeric receptor proteins comprising a single polypeptide chain of  
PT amino acids, useful as targets for drug actions, and as basis for drug  
PT discovery and development -  
XX  
XX  
PS Example 2; Page 55-56; 72pp; English.  
XX  
XX  
CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.  
CC The NPY receptors are G-protein-coupled transmembrane proteins with  
CC seven membrane spanning transmembrane (TM) domains. The compounds that  
CC modulate the activity of a NPY receptor is useful in the preparation of  
CC a medicament for treating conditions including obesity, high/low blood  
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,  
CC seizure, locomotor and anxiety disorders. They can also be used as  
CC targets for drug actions, and as basis for drug discovery and  
CC development. The NPY5 receptor may have an anti-epileptic activity in  
CC the control of limbic seizures. The present sequence is human NPY5  
CC receptor.  
XX  
XX  
SQ Sequence 455 AA;  
Query Match 90.9%; Score 1668.5; DB 22; Length 455;  
Best Local Similarity 73.2%; Pred. No. 7.3e-170;  
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 1 MSFYSKODYNMDELDEYYNKTATENNNTAATRNPDFVDDYKSSVDDQLQYFLIGLYTF 60  
Db 1 MSFYSKODYNMDELDEYYNKTATENNNTAATRNPDFVDDYKSSVDDQLQYFLIGLYTF 60  
QY 61 VSLIGFNGNLLIMALKKRNQKTYVNFILGNLAFSDILVLFCSPTLTSVLLDQMFEG 120  
Db 61 VSLIGFNGNLLIMALKKRNQKTYVNFILGNLAFSDILVLFCSPTLTSVLLDQMFEG 120  
QY 121 KVMCHIMPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFPLATVMTLGFAT 180  
Db 121 KVMCHIMPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFPLATVMTLGFAT 180  
QY 181 CSPLPVPHSLVELQETFGSALLSRYLCVSWPSDSYRIAFITSLLLVQYILPLVCLTVS 240  
Db 181 CSPLPVPHSLVELQETFGSALLSRYLCVSWPSDSYRIAFITSLLLVQYILPLVCLTVS 240  
QY 241 HTSVC-----IRLKRNNMMDK----- 257  
Db 241 HTSVCISISCSLGNKRELEENEMINLTLPKSKSGPOVLGSHKWSYFIKKHRRYS 300  
QY 258 -----MRQNKYR----- 264  
Db 301 KKTACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIPGVPCTCEIKPEENSDVHEL 360  
QY 265 -----SSRSRSVFRYLITILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 315  
Db 361 RVRKSVTRIKRSRSVFRYLITILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
QY 316 HLLGMSSCCLNPILYGLFNGIKADLVSLIHCLHM 350  
Db 421 HLLGMSSCCLNPILYGLFNGIKADLVSLIHCLHM 455  
RESULT 14  
ABB79510  
ID ABB79510 standard; Protein; 455 AA.  
XX  
XX  
AC ABB79510;  
XX  
XX  
DT 23-SEP-2002 (first entry)  
XX  
XX  
DE Human neuropeptide Y5 receptor.  
XX  
XX  
KM Neuropeptide Y5; NPY; NPY5; receptor; human; antagonist; anorectic;  
KM antiinflammatory; nootropic; neuroprotective; cardiovascular;  
KM hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiac;  
KM cerebroprotective; antidepressant; haemostatic; tranquillizer;  
KM

KM neuroleptic; analgesic; antianalgesic; nephrotoxic; uropathic;  
KM gastrointestinal; antistimulant.  
XX Homo sapiens.  
XX MO200248152-A2.  
XX 20-JUN-2002.  
XX 11-DEC-2001; 2001WO-US47863.  
XX 12-DEC-2000; 2000US-254990P.  
XX (NEUR-) NEUROGEN CORP.  
XX Baktavatchalam R, Blum CA, Brielmann HL, Darrow JM, De Lombaert S;  
PI Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;  
XX WPI; 2002-547845/58.  
XX DR N-PSDB; ABN84252.  
XX New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or  
PT 3H-spiroisobenzofuran-1,4'-piperidine, useful for treating, e.g. eating  
PT disorder, psychiatric, cardiovascular disorder or diabetes .  
XX Example 675; Page 129-130; 134pp; English.  
XX PS The present sequence is the protein sequence for the human  
CC neuropeptide Y5 (NPY5) receptor. In an example from the  
CC invention, chimeric receptors including human NPY5 receptor  
CC sequences, were constructed, and used to assay the binding  
CC activity of compounds of the invention. Substituted  
CC spiro(isobenzofuran-1,4'-piperidin)-3-ones and  
CC 3H-spiroisobenzofuran-1,4'-piperidines capable of modulating NPY5  
CC receptor activity are provided. Such compounds may be used to  
CC modulate ligand binding to NPY5 receptors in vivo or in vitro,  
CC and are particularly useful in the treatment of a variety of  
CC disorders, e.g. eating disorders such as obesity or bulimia,  
CC psychiatric disorders, diabetes and cardiovascular disorders such  
CC as hypertension, in humans and animals.  
XX CC  
XX Sequence 455 AA;  
SQ  
Query Match 90.9%; Score 1668.5; DB 23; Length 455;  
Best Local Similarity 73.2%; Pred. No. 7.3e-170;  
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60  
Db 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60  
QY 61 VSLGFGNLLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
Db 61 VSLGFGNLLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
QY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180  
Db 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180  
QY 181 CSPLPVHSHLVELOETFGSALLSRYLCVSPSDSRIATISLLVQYTLPLVCULTVS 240  
Db 181 CSPLPVHSHLVELOETFGSALLSRYLCVSPSDSRIATISLLVQYTLPLVCULTVS 240  
QY 241 HTSYVC---IRLKRNNMMDK----- 257  
Db 241 HTSYVCRIISGLSKNKRLEENEMINLTLHPSKSGPOVKLSGSHKKSYSFIKKHRRYS 300  
QY 258 -----MRDNKYR----- 264  
Db 301 KKTACVLPADERPSSQENHSHLPENFGSVRSQSSSKFTPGVPTCEIKPEENSVDHEL 360  
QY 265 -----SSRSRSVYRLTLITLILVFAVSWMPHLHFNVTDFPDNLISNRHKLVCIC 315  
|||||

Db 361 RYKRSVTRIKRRSRSEFYRLTLILVFAVSWMPHLHFNVTDFPDNLISNRHKLVCIC 420  
QY 316 HILGMSCCLNPILYGFNLNGIKADLVSLHCLHM 350  
Db 421 HILGMSCCLNPILYGFNLNGIKADLVSLHCLHM 455  
RESULT 15  
AAE08016  
ID AAE08016 standard; Protein: 455 AA.  
XX AAE08016;  
AC AAE08016;  
DT 01-NOV-2001 (first entry)  
XX African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.  
XX African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.  
KM Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
KM transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;  
KM Huntington's disorder; Parkinson's disorder; eating disorder; seizure;  
KM locomotor; anxiety disorder; limbic seizure; tranquilliser;  
KM african green monkey; AGM.  
XX Cercopithecus aethiops.  
XX OS  
XX WO200155103-A2.  
XX PD 02-AUG-2001.  
XX 29-JAN-2001; 2001WO-US02804.  
PF 28-JAN-2000; 2000US-0178652.  
PR (NEUR-) NEUROGEN CORP.  
XX PA Bennett M, Brodbeck R, Krause J;  
XX WPI; 2001-514543/56.  
DR N-PSDB; AAD14746.  
XX New chimeric receptor proteins comprising a single polypeptide chain of  
PT amino acids, useful as targets for drug actions, and as basis for drug  
PT discovery and development .  
XX PS Example 2; Page 70-72; 72pp; English.  
XX PS The present invention relates to chimeric neuropeptide Y (NPY) receptors.  
CC The NPY receptors are G-protein-coupled transmembrane proteins with  
CC seven membrane spanning transmembrane (TM) domains. The compounds that  
CC modulate the activity of a NPY receptor is useful in the preparation of  
CC a medicament for treating conditions including obesity, high/low blood  
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,  
CC seizure, locomotor and anxiety disorders. They can also be used as  
CC targets for drug actions, and as basis for drug discovery and  
CC development. The NPY5 receptor may have an anti-epileptic activity in  
CC the control of limbic seizures. The present sequence is african green  
CC monkey (AGM) NPY5 receptor.  
XX CC  
XX Sequence 455 AA;  
SQ  
Query Match 90.7%; Score 1665.5; DB 22; Length 455;  
Best Local Similarity 73.0%; Pred. No. 1.5e-169;  
Matches 332; Conservative 7; Mismatches 11; Indels 105; Gaps 3;  
QY 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60  
Db 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60  
QY 61 VSLGFGNLLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
Db 61 VSLGFGNLLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
QY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180

```

Db 121 KVMCHMPFLOCVSVLSTLILSLIAIARYHMIKHPISNNLTANHGFFLATVWTLGPAI 180
QY 181 CSPLPVPHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
Db 181 CSPLPVPHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSYC-----IRLKRNNMMDK----- 257
Db 241 HTSYCRSISCGLSNKENRENEMINLTHPSRKIGPOVKLSGSHKWSYSPFKKRRRYS 300
QY 258 -----MRDNKYYR----- 264
Db 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIPOVPTCEIKPENSDVHEL 360
QY 265 -----SSRSRSVFYRLTILILVFAVSWMPLLFHVVTDFENDNLISNRHFKLYYCIC 315
Db 361 RVKRSVTIRIKRRSRVFYRLTILILVFAVSWMPLLFHVVTDFENDNLISNRHFKLYYCIC 420
QY 316 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 350
Db 421 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

```

Search completed: November 22, 2002, 13:09:24  
 Job time : 40 secs

**This Page Blank (uspto)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:08:09 ; Search time 34 Seconds

(without alignments)  
2121.073 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836  
Sequence: 1 MSFYSKQDYNMDELDEYTN.....GLNLNGIKADVLNHLCHLM 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SP archaea:\*
- 2: SP bacteria:\*
- 3: SP fungi:\*
- 4: SP human:\*
- 5: SP invertebrate:\*
- 6: SP mammal:\*
- 7: SP mhc:\*
- 8: SP organelle:\*
- 9: SP phage:\*
- 10: SP plant:\*
- 11: SP rodent:\*
- 12: SP virus:\*
- 13: SP vertebrate:\*
- 14: SP unclassified:\*
- 15: SP yvirus:\*
- 16: SP bacteriaph:\*
- 17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1610.5	87.7	445	6	09GK73 macaca mula
2	1589.5	86.6	446	11	0925F1 macaca mula
3	1219	66.4	443	13	080FM2 macaca mula
4	644	35.1	383	6	09GK75 macaca mula
5	630	34.3	385	13	080FM1 macaca mula
6	617.5	33.6	377	13	073733 gallus gall
7	578	31.5	377	13	080GM3 gallus gall
8	554.5	30.2	374	13	080GM3 gallus gall
9	539	29.4	375	13	057463 brachydanio
10	531	28.9	365	13	08UW7 lampetra fl
11	518.5	28.2	375	6	097505 sus scrofa
12	515.5	28.1	373	13	073734 brachydanio
13	512	27.9	372	11	0922D4 cavia porce
14	503	27.4	381	11	09ERCO ratius norv
15	443.5	24.2	481	5	0967T7 drosophila
16	443.5	24.2	485	5	08S235 drosophila

17	429	23.4	600	5	09VW75 drosophila
18	415.5	22.6	475	5	09VNM1 drosophila
19	409	22.3	452	5	09VB87 drosophila
20	401	21.8	290	4	099463 homo sapien
21	395	21.5	336	5	09Y073 lymnaea sta
22	389	21.2	402	5	0964E5 dugesia tig
23	381	20.8	405	11	0924N0 mus musculu
24	378	20.6	465	5	044426 lymnaea sta
25	377.5	20.6	417	11	0924H0 mus musculu
26	375	20.4	540	5	09VRM0 drosophila
27	374	20.4	408	4	096RV1 homo sapien
28	370	20.2	429	5	P92045 lymnaea sta
29	368.5	20.1	422	11	08VHD7 rattus norv
30	366.5	19.9	432	11	0924G9 rattus norv
31	366	19.9	430	4	096RN3 homo sapien
32	362	19.7	412	5	020275 caenorhabd
33	358.5	19.5	436	11	08VCC7 mus musculu
34	357	19.4	365	5	09XXU4 caenorhabd
35	355.5	19.4	436	11	09DBV6 mus musculu
36	346.5	18.9	397	5	09NRA4 boophilus m
37	345.5	18.8	399	5	020067 caenorhabd
38	344	18.7	423	5	0964D4 periplaneta
39	342.5	18.7	431	5	08TBD1 urechis uni
40	341	18.6	357	5	09NBC8 drosophila
41	340.5	18.5	391	5	09GZ68 caenorhabd
42	335	18.2	394	5	09U721 drosophila
43	334	18.2	398	4	09UDE6 homo sapien
44	333	18.1	329	5	09VAU0 drosophila
45	332	18.1	361	5	08WPA2 bombyx mori

## ALIGNMENTS

### RESULT 1

ID	Q9GK73	PRELIMINARY	PRT	445 AA
AC	Q9GK73			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Neuropeptide Y receptor Y5.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;			
OC	Cercopitheciinae; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-21184974; PubMed-11287088;			
RA	Gehlert D.R., Yang P., George C., Wang Y., Schober D.,			
RA	Gackenhelmer S., Johnson D., Beavers L.S., Gadsdi R.A., Baez M.,			
RT	"Cloning and characterization of Rhesus monkey neuropeptide Y receptor			
RT	subtypes(1).";			
RL	Peptides 22:343-350(2001).			
EMBL	AF303091; AA640773.1;			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PRINTS: PR00237; GPCR_Rhodopsn.			
DR	PROSITE: PS50262; G_PROTEIN_REC2; 1.			
KW	Receptor.			
SO	SEQUENCE 445 AA; 50812 MW; AEDACD259675BC93 CRC64;			

Query Match 87.7%; Score 1610.5; DB 6; Length 445;  
Best Local Similarity 72.4%; Pred. No. 1.4e-128;  
Matches 32; Conservative 7; Mismatches 11; Indels 105; Gaps 3;

QY	11	MDLELDYNNKTATENNATATNSDPVWDYKSSVDDQLQYFLIGLYTEVSLGFGNLT 70
DB	1	MDLELDYNNKTATENNATATNSDPVWDYKSSVDDQLQYFLIGLYTEVSLGFGNLT 60
OY	71	LILMALKKRNQKTVVFLGNLAFLSDILVVLFCSPPTLISVLLDQMFKKVACHINPFL 130

Db 61 L1MALMKRRNOKTTVNFLLGNLAFSDLLVLFCSPTFLTSVLLDQMMFGKVMCHIMPEL 120  
Qy 131 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGAFCISPLPEVHSL 190  
Db 121 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGAFCISPLPEVHSL 180  
Qy 191 VELOETFGSALLSSRYLCVESWPSDYRIAFITISLLVQYILPLVCLTVSHTSVC-----I 246  
Db 181 VELOETFGSALLSSRYLCVESWPSDYRIAFITISLLVQYILPLVCLTVSHTSVCISIC 240  
Qy 247 RLKRRNNMMDK----- 257  
Db 241 GLSNKENRLEENEMINLTLHPSRKIGPOVKLSGSHKWSYFIKKIRRKSKKTACVLPAP 300  
Qy 258 ---MRDNKYR-----S 265  
Db 301 ERPSQENHSRILPENFGSVRSQISSSKFIPGVPTCFEIKPEPNSDVHELRYKRSVTRIK 360  
Qy 266 SRSRSVFYRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 325  
Db 361 KRSRSVFYRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 420  
Qy 326 NPILYGFLLNGIKADLVSLIHCLHM 350  
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

## RESULT 2

Q925F1 PRELIMINARY; PRT; 446 AA.  
AC Q925F1;  
DT 01-DEC-2001 (TReMBUrel. 19, Created)  
DT 01-DEC-2001 (TReMBUrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBUrel. 20, Last annotation update)  
DE Npy receptor 5.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviiidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184976; PubMed=11287090;  
RA Lundell I., Eriksson H., Marklund U., Larhammar D.;  
RT "Cloning and characterization of the guinea pig neuropeptide y  
receptor Y5.";  
RL Peptides 22:357-363(2001).  
DR EMBL: AF363240; AAK52800.1; -.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE: PSS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 446 AA; 50936 MW; 2C3984B0A90AA693 CRC64;

Query Match 86.6%; Score 1589.5; DB 11; Length 446;  
Best Local Similarity 71.5%; Pred. No. 8.6e-127;  
Matches 318; Conservative 9; Mismatches 13; Indels 105; Gaps 3;

Qy 11 MDLEDEYNNKTATENNATATRNSDPEVMDYKSSVDDIYFLIGLYTFVSLGFMGNL 70  
Db 1 MDLELKEYNNKTATENNATATRNSDPEVMDYKSSVDDIYFLIGLYTFVSLGFMGNL 60  
Qy 71 L1MALMKRRNOKTTVNFLLGNLAFSDLLVLFCSPTFLTSVLLDQMMFGKVMCHIMPEL 130  
Db 61 L1MALMKRRNOKTTVNFLLGNLAFSDLLVLFCSPTFLTSVLLDQMMFGKVMCHIMPEL 120  
Qy 131 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGAFCISPLPEVHSL 190  
Db 121 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGAFCISPLPEVHSL 180  
Qy 191 VELOETFGSALLSSRYLCVESWPSDYRIAFITISLLVQYILPLVCLTVSHTSVC----- 245  
Db 181 VELOETFGSALLSSRYLCVESWPSDYRIAFITISLLVQYILPLVCLTVSHTSVCISIC 240

Qy 246 -----IRL-----KRRNNMMDKRDKNKYSS----- 266  
Db 241 GLSNKENRLEENEMINLTLHPSRKGQVQLSKTHKWSYFIKKIRRKSKKTACVLPAP 300  
Qy 267 ----- 266  
Db 301 ARPSLENSRFLPENFGSVRSQISSSKFIPGVPTCFEIKPEPNSDAHEMRKRSITRIK 360  
Qy 267 -RSRSVFYRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 325  
Db 361 KRSRSVFYRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 420  
Qy 326 NPILYGFLLNGIKADLVSLIHCLHM 350  
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

## RESULT 3

O8QFM2 PRELIMINARY; PRT; 443 AA.  
AC O8QFM2;  
DT 01-JUN-2002 (TReMBUrel. 21, Created)  
DT 01-JUN-2002 (TReMBUrel. 21, Last sequence update)  
DT 01-JUN-2002 (TReMBUrel. 21, Last annotation update)  
DE Neuropeptide y receptor Y5.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Holmberg S.K.S., Mätkö S., Boswell T., Zoorob R., Larhammar D.;  
RT "Pharmacological characterization of cloned chicken neuropeptide y  
receptors Y1 and Y5.";  
RL J. Neurochem. 81:462-471(2002).  
DR EMBL: AY040844; AAK83556.1; -.  
KW Receptor.  
SQ SEQUENCE 443 AA; 50044 MW; EPE9F1A391CC092E CRC64;

Query Match 66.4%; Score 1219; DB 13; Length 443;  
Best Local Similarity 55.5%; Pred. No. 2.1e-95;  
Matches 246; Conservative 35; Mismatches 52; Indels 110; Gaps 6;

Qy 11 MDLEDEYNNKTATENNATATRNSDPEVMDYKSSVDDIYFLIGLYTFVSLGFMGNL 70  
Db 1 MDLGFQDVTNRT-PTKNTSATTKN--FSAWEDYSSVDDIYFLIGLYTLLISLAGFYGNL 57  
Qy 71 L1MALMKRRNOKTTVNFLLGNLAFSDLLVLFCSPTFLTSVLLDQMMFGKVMCHIMPEL 130  
Db 58 L1LVAL-TKRQKTIINILGNLAFSDLLVLFCSPTFLTSVLLDQMMFGKVMCHIMPEL 116  
Qy 131 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGAFCISPLPEVHSL 190  
Db 117 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGAFCISPLPEVHSL 176  
Qy 191 VELOETFGSALLSSRYLCVESWPSDYRIAFITISLLVQYILPLVCLTVSHTSVCIRLKR 250  
Db 177 VDLKRTLNLKLENRRLCIESWPSDYRIAFITISLLVQYILPLVCLTVSHTSVCISVGS 236  
Qy 251 R-----NNMD----- 256  
Db 237 RLSSKEGFOENEMINLTLHPSKSAGTEAQPSSHTSMSCALVRKHRRYSKSTVMPAI 296  
Qy 257 ---KMRDNKYR----- 264  
Db 297 LRQQODADFDLPTSGTEKSQSSSKFIPGVPICEMKPEENTEIOMITVSQSIIRI 356  
Qy 265 SRSRSVFYRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCC 324  
Db 357 KTRRRRYFCRLTVLLIVFGSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCC 416  
Qy 325 LNPILYGFLLNGIKADLVSLIHCLHM 347

[illegible][illegible]

RX MEDLINE=99337783;  
 RA Starback P., Lundell I., Fredriksson R., Berglund M.M., Yan Y.L.,  
 RA Wraith A., Soderberg C., Postlethwait J.H., Larhammar D.,  
 RT "Neuropeptide y receptor subtype with unique properties cloned in the  
 RT zebrafish: the zya receptor";  
 RL Brain Res. Mol. Brain Res. 70:242-252(1999).  
 DR EMBL; AF037400; AAC41276.1; -;  
 DR HSSP; P02699; 1F88.  
 DR ZFIN; ZDB-GENE-980526-393; npdyra.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW Receptor.  
 SO SEQUENCE 377 AA; 42901 MW; 60E62AD9C7BFEE5D0 CRC64;

```

Query Match          33.6%  Score 617.5: DB 13; Length 377;
Best Local Similarity 37.1%: Pred. N1.7e-44;
Matches 124; Conservative 66; MisMatches 133; Indels 11; Gaps

QY      20  NKTLTENNATATRRNSDFPMDYKSSVDLDLYFLIGLTYFSLICGFOMNLITLMAIMKK 79
Db      16  NSTLTHNQSNSLFLDDPWC---QSSITFL--LVLCGLVLILGLLNLITLICIMIQ 70
QY      80  RNQKTYVFLIGNLAFSDILVVLVFCSPFTLTJSLVDLDMNKGKVMCHIMFLQCVSLYMT 139
Db      71  RDPNVTWITILLANLSVDSDILVSVFCPLPFTVYVTLMDHMFGLALCRLMPFQCVSVTSV 130
QY      140  LILISIAIVRYMIMKHPISSNNLTANHGFLLITVMTLGRATSPRLVPSLYELOETFGS 199
Db      131  LSLVIAIERHOLILHPSGMKPSVQAVIAYLVLTWMLLACVTSYLPFLAFILLTSEPSLTP 190
QY      200  ALLSRRYLCVESMPDSRYIAFTISLLIYOYLITPVLCVLSVTSYICRLKRNNMMDKM- 258
Db      191  APLSOLOVCLEWPSQDHRKLAATTSSLLLFQYCCPLMLLCTYRIFRLQRRERMIERCC 250
QY      259  ----RDNKYRSSRSRSVFEYRLTILLVAVSMRPLHFEHVYVDFNDNLISNHFKLUVCI 314
Db      251  SRNREDEHRRVYHSHKRINVMYLAATLVAARFAYCLRLNIAFNVVADQGEVLPVCSNHNLSFL 310
QY      315  CHLLGMSCCLNPLIYLGFNLNGIKRDLVSLI-HC 347
Db      311  CHLLAMSTCVNPIIYLGFLNSNFRDVAVSVLHC 344

```

RESULT 7			
ID	ORGSM3	PRELIMINARY;	PRT; 377 AA.
AC	ORGSM3;		
DT	01-JUN-2002 (TREMBLrel, 21, Created)		
DT	01-JUN-2002 (TREMBLrel, 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel, 21, Last annotation update)		
DE	Neuropeptide Y receptor 4.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauromia; Aves; Neognathae; Galliformes; Psittacidae; Psittacineae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lundell T., Boswell T., Larhammar D.;		
RT	"Chicken Neuropeptide Y Family Receptor Y4; a Receptor with Equal		
RT	Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY."		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF110853; ALA84161.1; -.		
KM	Receptor.		
QO	SEQUENCE 377 AA; 42972 MW; C9EC6C00DBFD1P9E CRC64;		

Query Match	31.5%	Score 578	DB 13	Length 377
Best Local Similarity	34.6%	Pred. No. 3.9e-41		
Matches 119	Conservative 78	Mismatches 129	Indels 18	Gaps 8

```

0Y 20 NKILATE-----NNTAATRNSDPFV-WDDYKSSVDDLDQYFLIGLYTFSLLGEMGNLI 72
      |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 2 NKTRAVHDAFPFLNNKNNLSNRSFSLNSDCCRNTDLTVELATSYSELYGIVGNCL 61
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
0Y 73 LMALEKKRNRKQKTYVFLGNLAFSPIILVFCPSPTTSLVDDOMGEKVMCHMPLLOC 133
      :  :  :  :  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 62 IAVIRKQEKTNVTNILLNSLISDLEMCVLCPETVYTYMDWYHGEVNMCKMTSTQOC 122
      :  :  :  :  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
0Y 133 VSVLSTPLILSLIAVIRAHMTKHPISNNLTANHGFIATWATGFCALCSPDPEHSHV 191
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 122 TSVTYSLISLVIALERQQLIINPTGMRPSISQAYLGIVGTYWL-ACLSMLPFLTYSIL 175
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
0Y 192 --ELQETFGSALLSRY--LCQVSPSDSYRIAFTISLLVLQYILPLVCLTYSHTSVCI 246
      :  :  :  :  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 180 SMDLEEQ-LSHIMNFSYDKAICIDISMPSEQRLLIYTTLLTLQXCIPLFIITLCYLRIL 238
      :  :  :  :  :  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
0Y 247 RLKRRNNMMQMKRDNKYASSRSRSYFRKLTLLILVFAVSMMPLLPHVYVDENDNLISNR 306
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 239 RLOKRRKDMFEK-SEYSNRAVODLRIRNILLASMAVAFAVCMBPLHVFNTYDMNMYKIISPC 297
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
0Y 307 HFKLYCYCHLLGMSCCLNPLINGFLANGIKADLYSLI-HCLH 349
      ||  :  :  :  |||  ||  :  :  :  |||  ||  :  :  :  |||  ||  :  :  :
Db 298 HHNLFSLCHLYAAMASTCVNPVLYTGFLNSNRKKKXSLISQCH 341
      ||  :  :  :  |||  ||  :  :  :  |||  ||  :  :  :  |||  ||  :  :  :

```

RESULT 8	Q9YHX1	PRELIMINARY:	PRT:	374 AA.
ID	Q9YHX1			
AC	Q9YHX1;			
DT	01-MAY-1999 (Tremblrel. 10, Created)			
DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)			
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)			
DE	Neuropeptide Y/peptide YY receptor Yb.			
GN	NPYR1			
OS	Gadus morhua (Atlantic cod).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.			
OX	NCBI_TaxId=8049;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99017378; PubMed=9802392;			
RA	Arvidsson A.K., Wralth A., Jonsson-Rylander A.C., Larhammar D.;			
RT	"Cloning of a neuropeptide Y/peptide YY receptor from the Atlantic			
RT	cod: the yb receptor.";			
RL	Regul. pept. 75:39-43(1998).			
DR	EMBL: AF073925; AADD2833.1; -			
DR	Interpro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PS00237; GPCRHHODPSN.			
DR	PROSITE: PS00237; G_PROTEIN_RECPT_FL1; UNKNOWN_1.			
DR	PROSITE: PS50262; G_PROTEIN_RECPT_FL2; 1.			
QJ	SEQUENCE 374 AA: 42260 MW: D2A9C9516C4998E2 CRC64:			

Query Match:	30.2%	Score 554.5:	DB 13:	Length 374:
Best Local Similarity:	35.2%	Pred. NO. 3.7e-39:		
Matches 108, Conservative	67:	Mismatches 113:	Indels 19:	Gaps 5

```

QY 53 FLIGLVEVSLGEGMGLILMALMKRKNQKTTVNFILGNLAFSDILVYFCSEFTLSV 112
    ||| : : : : : : : : : : | : : : : : : : : : : | : :
Db 39 FLILVYSTMILAVGIVGNSCLVEFIARKEKHNTNPIELMSCDILMCIJFCPLVTLIYT 98
    ||| : : : : : : : : : : | : : : : : : : : : : | : :
QY 113 LLDQMFGKVMCHIMPFQCSVLYSLILISTAIIVYHMKIKHPIISNNLTANHCYFLIAT 172
    ||| : : : : : : : : : : | : : : : : : : : : : | : :
Db 99 LMDRMILGEALCKLTPVQCISIVSVSIFSLVLAMERYQOLIHPTGKPMVGOSYMAVGI 158
    ||| : : : : : : : : : : | : : : : : : : : : : | : :
QY 173 VMT-----LGFALCSPLPVFHSVLVEQGFPGSALLSRYLCVBSWPSDSYRAFTI 223
    ||| : : : : : : : : : : | : : : : : : : : : : | : :
Db 159 IMVYACILSVPELSFTYLDNLP-----IQNLSLPPGG--ODHWICRESMPTNSRLAYTT 211
    ||| : : : : : : : : : : | : : : : : : : : : : | : :
QY 224 SLLVQYILPLVCLTVSHTSVCILKRRNMMDMKRKNK--YRSRSRSFYRLTILILV 261
    ||| : : : : : : : : : : | : : : : : : : : : : | : :

```



Db 212 SLVFGYFLPLGLIACYLISFLRLARRKDMVERARDSSRDNRKSGRRINWMLGSLVAL 271

QY 282 FAVSWMPRLHLFHVVTDFENDNLISNRHFKLYVCICHLGLGMSCLLPILYGLNIGKADL 341

Db 272 FAVSWMPRLNLFNFVDMHHELVMSQCHNLIFSCHLVAMASTCVNPVYVGLNSNQKOL 331

QY 342 -VSLIHC 347

Db 332 KATLSHC 338

RESULT 9

057463 PRELIMINARY: PRT: 375 AA.

ID 057463

AC 057463; 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

GN Neuropeptide Y /peptide Y receptor YD.

NPYRB.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Lundell I., Berglund M.M., Starback P., Salaneck S., Gehlert D.R., Larhammar D.;

RT "Cloning and characterization of a novel neuropeptide Y (NPY) receptor subtype in the zebrafish.";

RL DNA Cell Biol. 0:0-0(1997).

DR EMBL: AF030245; AAB94616.1; -

DR ZFIN: ZDB-GENE-980526-208; npyrb.

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1

DR PRINTS: PR00237; GPCR\_RHODOPS.

DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_FL\_1; UNKNOWN\_1.

DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_FL\_2; 1.

KW Receptor.

SQ SEQUENCE 375 AA; 42116 MW; 4B0C9551131A14D1 CRC64;

Query Match 29.4%; Score 539; DB 13; Length 375;

Best Local Similarity 33.8%; Pred. No. 7.7e-38;

Matches 101; Conservative 68; Mismatches 122; Indels 8; Gaps 3;

QY 53 FLTGLTTPVSLGFMGNLLIIMALKKRNKQTVNPLIGLAFSDILVYFCSPFTLTSTV 112

Db 27 FLTVAISTMLAVGLVGTCLVAVITRQKERNVNTNIFVNLSCSDILVCLVCLPVTIYTP 86

QY 113 LLDQMGFKVMCHIMPELOCVSVLSTLLISIAIVRYHMKRPNISNLTANHGYPFIAT 172

Db 87 LMDRWTLGELALCKVTPFVOCMSVTVSIFSMVLALERHQLIHPTGKRPVRRHSYLAVAL 146

QY 173 VMTLGAISPLRPFHSLV-----LQETFGSALLSSRYICVSPSDSYRIAFYISLL 227

Db 147 IWTIACFISLPFLSFNLTNSPFNLSLPFN--FSDHFECIQOWSEGNRLTYTTLL 204

QY 228 VOYIILVLCVTSHTSVCIIRKRRNMMDKMRNKKYRSSR-SRSVYRLLIILLVAVSW 286

Db 205 CQYCLPLALVLCYFRIFLISRRKDMVERARGROKKAAGSRVNAAMLASIVAALFLCW 264

QY 287 MPLHLFHVVTDFENDNLISNRHFKLYVCICHLGLGMSCLLPILYGLNIGKADVSLI 345

Db 265 LPLNVENTFTFDMNHDAIPVQCHDAIFSACHLTMASTCVNPVYVGLNNSNQKOLSL 323

RESULT 10

ID 08UVW7 PRELIMINARY: PRT: 365 AA.

AC 08UVW7; 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE NPY receptor.

OS Lampetra fluviatilis (River lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Lampetra.

OX NCBI\_TaxID=7748;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21590343; PubMed=11733009;

RA Salaneck E., Fredriksson R., Larson E.T., Conlon J.M., Larhammar D.;

RT "A neuropeptide Y receptor Y1-subfamily gene from an agnathan, the European river lamprey, A potential ancestral gene.";

RL Eur. J. Biochem. 268:6146-6154(2001).

DR EMBL: AF340022; AAL66410.1; -

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_RHODOPS.

DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_FL\_1; UNKNOWN\_1.

DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_FL\_2; 1.

KW Receptor.

SQ SEQUENCE 365 AA; 41060 MW; 9EE5FD3BBE6807E9 CRC64;

Query Match 28.9%; Score 531; DB 13; Length 365;

Best Local Similarity 34.1%; Pred. No. 3.6e-37;

Matches 110; Conservative 66; Mismatches 135; Indels 12; Gaps 5;

QY 35 SDFPVMD-DYKSSVDDLYFLIGLYTFVSLGFMGNLLIIMALKKRNKQTVNPLIGNL 93

Db 10 SEMRQDLDDHCQRPQAVRSVIAVTCVLIAGLGNLSLVLYLRSELNWNILVNL 69

QY 94 AFSDILVYFCSPFTLTSTVLLDQMGFKVMCHIMPELOCVSVLSTLLISIAIVRYHMT 153

Db 70 AFSDMLVGLCLPLTLIATVLTMDHMFGEALCKGSPLOCASVSISFLVIAIERHQLI 129

QY 154 KHPISNLTANHGYPFIATVYVTLGFAICSPLPVHSLVE-----LQETFGSALLSSRYIC 208

Db 130 INPTGKFPSLNHAIVAGALVAAFAWSSPFLAHVLTDEPRNLSHYFPD--YGEKVAC 187

QY 209 VESWPSDSYRIAFYISLLAVQYILPVCLTVSHTSVCIRKRRNMMDKKRD--NKYRS 265

Db 188 IEVVALGHLKFAFTTSLTLVQFSCPLFLVFLCYLRFLRQKKMLPTRGBGQNVRA 247

QY 266 SRSRSVFYRLLIILVAVSWMPRLHLFHVVTDFENDNLISNRHFKLYVCICHLGLGMSCL 325

Db 248 SHMKKIMMLVAIVAGFAICMLPLTYFNVAWSNPTLLHCOHDLIFSCHLTAMLSICI 307

QY 326 NPLTYGLNIGKADL-VSLIHC 347

Db 308 NPLTYGLNINPLKELKATILLRC 330

RESULT 11

ID 097505 PRELIMINARY: PRT: 375 AA.

AC 097505; 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN Neuropeptide Y receptor type 4 (Neuropeptide Y-family receptor Y4).

NPY Y4.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=LMD; TISSUE=KIDNEY;

RT Ito Y., Minezawa M.;

RT "Sus scrofa NPY Y4 gene for neuropeptide Y receptor type 4, complete cds [genomic]";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RN [2]



```

DR PROSITE, PSS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
SQ SEQUENCE 372 AA; 41774 MW; 5B6CF78FB213374 CRC64;

Query Match 27.9%; Score 512; DB 11; Length 372;
Best Local Similarity 31.1%; Pred. No. 1.5e-35;
Matches 103; Conservative 73; Mismatches 139; Indels 16; Gaps 4;

QY 22 TLATENNTAARNSDPFWDDYKSSVDDLDQYFLGLGIVFVSLGFGMLILMALMKRN 81
D 13 TYRPEENSKRQRLFN-FSDHCODSGDLMEFIVSYGEFIVGVGLNCLITMLRQKE 71
QY 82 QKTVNFIQLNALFSDIILVLLFCSPFTLLSVLLDQMGFKWCHIMPLQCVSLVSTLI 141
D 72 KANVTSLILMALFSDFLMLCLICQPLFVIYTIMDWIGEVGLCKMSAFIQCSMTVSILS 131
QY 142 LLSIAIVYHHKIKRPIISNNLTANHCYFLFLLATVWTLGFRFICSL-----PVHSLVELQ 194
D 132 LVLALEHHQILINPTGKKPSVPQAYLGIVATLIVMLIACVLSLREPLANSILENPFH- ---N 187
QY 195 ETPFSALLSRYLCEVSPSDSYRAETFLISLVQYLRLPCLVYSHTSVCIRLKRNM 254
D 188 HSKALAFLEDKVACKESRPLGNHRRVYTFLLRQYCRPLAFILVCYLIRSLRRLRQGRV 247
QY 255 MDKMRDNKRSSRSRSRYEYRLTLLVFAVSMPLRFLHVVYTFENDNLSINRHFLLVYCI 314
D 248 LCK-----SSRAGMKRIRGVLVAMGAVARLMLPLHVENSLIEDMHEALPCHGNLIFLV 303
QY 315 CHLGMMSCCLPILYGLFLNNGIKADVSLI 345
D 304 CHLLAMASTCVNPFYGLFLNTNFKKEVALV 334

RESULT 14
Q9ERCO
ID Q9ERCO PRELIMINARY; PRT; 381 AA.
AC Q9ERCO;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Neuropeptide Y/peptide YY-Y2 receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Sciuriata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=SMALL INTESTINE;
RA Volin T., Goumain M., Laburthe M.;
RT "Cloning of a cDNA encoding a rat type 2 neuropeptide Y/peptide YY
RT receptor expressed in intestinal epithelial crypt cells.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY004257; AAF89094.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR001220; Lectin_legb.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PRINTS: PR01570; NPFFRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECPE_FL_1; UNKNOWN_1.
DR PROSITE: PS30262; G_PROTEIN_RECPE_FL_2; 1.
DR PROSITE: PS00307; ECTTN_LEGUME_BETA; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 381 AA; 42510 MW; 6593272904B288BC7 CRC64;

Query Match 27.4%; Score 503; DB 11; Length 381;
Best Local Similarity 32.2%; Pred. No. 8.8e-35;
Matches 98; Conservative 75; Mismatches 117; Indels 14; Gaps 5;

QY 49 DLOEFLGLYFVSVLISGMNLLIMALKRKNQKTVNPLIGNLAFSDIILVLLFCSPFT 108
D 48 EVQVYVLLIATYSIILLGVGNSLVIVHYIKRSMRTYTNFPLANLAVDELIVNTLCPEPT 107
QY 109 LTVSLLDQMGFKWCHIMPLQCVSLVSTLILISIAIVRYHMKIKRPIISNNLTANHCYF 168

```

Dd		108	LFTYLMGEEKMGPVCLCHLVPYAQGLAVOVSTTLTVIALDRHRCIVLYHLESKIISOISLT	167
Oy		169	LTAATYTGCFAICSPPLPVE--HSVLDEQTFSCSALLSRYLCEVESMPDS--YRIAPT	223
Dd		168	IIGLAMGVASALLASPLAIFREYSLEIIPDF-----ELVACTEWMPEGEKSVGTYSL	221
Oy		224	SLLLVQYILPLVCLVTSHTSVCIRLKRRNNMDKMRDNKRSSRSRVSFYLRTILLVFA	283
Dd		222	STLLLVLPVLPGLIISEFSYTRIMSKLK--NHVSPGAASHDHQRHRKHTT-KMLVCVVVFA	278
Oy		284	VSMPLHLHFHVYTFDNDLSINRHKRYVICIHLGMSCCNPLLGYFLNNGICADIVS	343
Dd		279	VSMPLHLAFOLAVDDSDSHVLDEKRLIFTVFHIAMCSTFANPLLGMWNSNYRAFLS	338
Oy		344	LHC 347	
Dd		339	AERC 342	
 RESULT 15 096777				
ID	096777	PRELIMINARY:	PRT:	481 AA.
AC	096777			
DT	01-DEC-2001	(TREMBREL 19, Created)		
DT	01-DEC-2001	(TREMBREL 19, Last sequence update)		
DP	01-JUN-2002	(TREMBREL 21, Last annotation update)		
DE		Neuropeptide F receptor.		
GN	NPFRL OR CG1147.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_taxid=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Garczynski S.F., Jr., Brown M.R., Shen P., Murray T.F., Cline J.W.;			
RT	"Characterization of a functional neuropeptide F receptor from			
RL	Drosophila melanogaster."			
DR	Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF364400; AAK50050.1; -			
DR	Flybase; FBgn0037408; NPFRL			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR01570; NPFRRECEPTOR.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.			
KW	Receptor.			
SQ	SEQUENCE 481 AA; 53092 MW; 9658EE900028CE8 CRC64;			
 Query Match 24.2%; Score 443.5; DB 5; Length 481; Best Local Similarity 31.2%; Pred. No. 1.2e-29; Matches 107; Conservative 72; Mismatches 135; Indels 29; Gaps 9;				
Oy		28	NATAATRNDSF-----PVWD--YKSSVDLDQY-FLIQLTYFVSLGFMGNIILM	74
Dd		46	NNTAINTSGDLNETGSRPDLPVIDRFELSRAVDSPWHNLIMSYGVLLFYEGALGMTVIYI	105
Oy		75	ALMKRRNQTTVNPILGNLASDIIVLFECSPFTLVSLDDOMFG--KWCMHPFILOC	132
Dd		106	AVIRKPRIKRTANFLFILMAISDLLCLVTMLMEILISKWPYGSCSIDLKTIAMLOA	165
Oy		133	VSVLSTLILSIALIVRHMIKHPISSNNLTANHGFILATVWTGLFALCSPLPFFHSIVE	192
Dd		166	LCIEVSTISITAIADRTOIVYPPRDSIQFPYGAVTIIGAILWALLASPLPYIKELI-	224
Oy		193	LOEFPGSALLSRYL-----CVESMPDSYRIAFTISILLVQYILPLVCLVSHTSVCI	246
Dd		225	--NTDTPALLOQIGLODTPICYIEDMPSNGRFFSYSIFSICQYIVLPIIVSAVAFGIYN	282
Oy		247	RLKRRNNMMDKMRDNKYTS-SRSRSVFTRLTI--LVFAVSMPLHLHFHVYTFDNDNL	302
Dd		283	RLKSITVIAVOASSAQKVERGRMRKRTNCLISIAIFGSVMPLNFENFLYADAMERSP	342



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:05:43 ; Search time 14 Seconds

(without alignments)  
1036.908 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836

Sequence: 1 MSFYSKQDYNMDELDEYYN.....GFLNGIKADLVSLHCLHM 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1668.5	90.9	455	1	NP5R_HUMAN
2	1581.5	86.1	446	1	NP5R_CANFA
3	1536	83.7	456	1	NP5R_RAT
4	1534.5	83.6	446	1	NP5R_PIG
5	1514.5	82.5	466	1	NP5R_MOUSE
6	650	35.4	382	1	NP5R_CANFA
7	650	35.4	383	1	NP5R_PIG
8	644	35.1	384	1	NP5R_HUMAN
9	640.5	34.9	383	1	NP5R_CANFA
10	637	34.7	366	1	NP5R_XENLA
11	633.5	34.5	382	1	NP5R_MOUSE
12	633.5	34.5	371	1	NP5R_RABIT
13	576.5	31.4	371	1	NP5R_MOUSE
14	552.5	30.1	371	1	NP5R_MOUSE
15	525	28.6	385	1	NP5R_CHICK
16	515.5	28.1	375	1	NP5R_MOUSE
17	515	27.5	375	1	NP5R_HUMAN
18	505.5	27.5	375	1	NP5R_RAT
19	505	27.5	381	1	NP5R_CANFA
20	504	27.5	381	1	NP5R_HUMAN
21	503	27.4	385	1	NP5R_MOUSE
22	501	27.3	384	1	NP5R_BOVIN
23	497	27.1	381	1	NP5R_MACMU
24	496	27.0	382	1	NP5R_PIG
25	464	25.3	370	1	NP5R_HUMAN
26	453.5	23.0	370	1	NP5R_RAT
27	421.5	23.0	449	1	NP5R_DROME
28	397.5	21.7	455	1	NP5R_XENLA
29	380.5	20.7	432	1	NP5R_RAT
30	378.5	20.6	423	1	NP5R_HUMAN
31	377.5	20.5	417	1	NP5R_RAT
32	375.5	20.4	453	1	NP5R_XENLA
33	374	20.4	522	1	NP5R_HUMAN

34	372.5	20.3	422	1	GP72_CANFA
35	366	19.9	430	1	NP5R_HUMAN
36	365.5	19.9	423	1	GP72_MOUSE
37	361.5	19.7	427	1	NP5R_RABIT
38	358.5	19.5	436	1	NP5R_MOUSE
39	354	19.3	444	1	NP5R_RAT
40	344.5	18.8	349	1	NP5R_HUMAN
41	341	18.6	346	1	NP5R_RAT
42	341	18.6	430	1	NP5R_CANFA
43	339	18.5	444	1	NP5R_HUMAN
44	337	18.4	348	1	NP5R_MOUSE
45	337	18.4	460	1	NP5R_RAT

#### ALIGNMENTS

RESULT 1  
ID NP5R\_HUMAN STANDARD; PRT; 455 AA.  
AC 015761; Q92916;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5 receptor) (NPY5)  
GN NP5R OR NPYR5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hippocampus;  
RX MEDLINE=96317589; PubMed=8700207;  
RA Gerald C., Walker M.W., Ciscione L., Gustafson E.L., Laz T.M., Batzli-Hartmann C., Smith K.E., Vayssie P., Durkin M.M., Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G., Taber R.I., Branchek T.A., Weinschenk R.L.;  
RA "A receptor subtype involved in neuropeptide-Y-induced food intake,"  
RT Nature 382:168-171(1996).  
RL [2]  
RP SEQUENCE OF 11-455 FROM N.A.  
RX MEDLINE=96421636; PubMed=8824284;  
RA Hu Y., Bloemquist B.T., Cornfield L.J., Decart L.B., Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L., Sedlowski Y., Schaefer J., Velazquez N., McCabe M.L.;  
RA "Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior,"  
RT J. Biol. Chem. 271:26315-26319(1996).  
RN [3]  
RP SEQUENCE OF 11-455 FROM N.A.  
RX MEDLINE=97312686; PubMed=9169127;  
RA Herzog H., Darby K., Ball H., Hort Y., Beck-Sickingler A., Shine J.;  
RT "Overlapping gene structure of the human neuropeptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation,"  
RL Genomics 41:315-319(1997).  
CC - FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS.  
CC - TISSUE SPECIFICITY: BRAIN; HYPOTHALAMUS.  
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```

CC -----
DR EMBL: U56079; AAC50623.1; -
DR EMBL: U66275; AAC50741.1; -
DR EMBL: U94320; AAC51295.1; -
DR GenBank: HGNC:7958; NPY5R.
DR MIM: 602001; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 51 72 1 (POTENTIAL).
FT DOMAIN 73 84 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 125 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 126 147 3 (POTENTIAL).
FT DOMAIN 148 167 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 168 188 4 (POTENTIAL).
FT DOMAIN 189 220 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 221 242 5 (POTENTIAL).
FT DOMAIN 243 321 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 321 401 6 (POTENTIAL).
FT DOMAIN 402 414 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 415 438 7 (POTENTIAL).
FT DOMAIN 439 455 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 124 208 BY SIMILARITY.
FT LIPID 452 452 PALMITATE (POTENTIAL).
SQ SEQUENCE 455 AA; 51990 MW; 95F2747E5FB8F7 CRC64;

```

```

Query Match 90.9%; Score 1668.5; DB 1; Length 455;
Best Local Similarity 73.2%; Pred. No. 6.1e-96;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

```

```

QY 1 MSFYSKQDYNNDELDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLOLYFLGLGYTF 60
DB 1 MSFYSKQDYNNDELDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLOLYFLGLGYTF 60
QY 61 VSLIGFMGNLLILALMAKRNQKTTVNFILGNLAFSDLLVLFCSPTFLTSVLDQWNG 120
DB 61 VSLIGFMGNLLILALMAKRNQKTTVNFILGNLAFSDLLVLFCSPTFLTSVLDQWNG 120
QY 121 KVMCHIMFLOCVSVLTLISLAIYRYHMIRKIPISNNLTANGYFLIATVMTLGFAL 180
DB 121 KVMCHIMFLOCVSVLTLISLAIYRYHMIRKIPISNNLTANGYFLIATVMTLGFAL 180
QY 121 KVMCHIMFLOCVSVLTLISLAIYRYHMIRKIPISNNLTANGYFLIATVMTLGFAL 180
DB 121 KVMCHIMFLOCVSVLTLISLAIYRYHMIRKIPISNNLTANGYFLIATVMTLGFAL 180
QY 181 CSPLPVHSLVELOETFGSALLISRYLCVESWPSDYRIAFETISLLVOYTLPLVCLTVS 240
DB 181 CSPLPVHSLVELOETFGSALLISRYLCVESWPSDYRIAFETISLLVOYTLPLVCLTVS 240
QY 241 HTSYC---ILKRRNNMMDK----- 257
DB 241 HTSYC---ILKRRNNMMDK----- 257
QY 241 HTSYC---ILKRRNNMMDK----- 257
DB 241 HTSYC---ILKRRNNMMDK----- 257
QY 258 -----MRDNKRR----- 264
DB 258 -----MRDNKRR----- 264
QY 301 KKTACVLPAPERPSOEINSRLLPENFGSVRSQSSSFICGVPTCFIKREBNSDVHEL 360
DB 301 KKTACVLPAPERPSOEINSRLLPENFGSVRSQSSSFICGVPTCFIKREBNSDVHEL 360
QY 265 -----SSRSNSVRYRLTLILVFAVSWMPLHLFHVYTDNFNDNLISNRHFKLVYIC 315
DB 265 -----SSRSNSVRYRLTLILVFAVSWMPLHLFHVYTDNFNDNLISNRHFKLVYIC 315
QY 361 RVKRSVTRIKRRSRVSFVRLTILVFAVSWMPLHLFHVYTDNFNDNLISNRHFKLVYIC 420
DB 361 RVKRSVTRIKRRSRVSFVRLTILVFAVSWMPLHLFHVYTDNFNDNLISNRHFKLVYIC 420
QY 316 HLLGMSCCLNPILYGLFNNGIKADVSLHCLHM 350
DB 316 HLLGMSCCLNPILYGLFNNGIKADVSLHCLHM 350
QY 421 HLLGMSCCLNPILYGLFNNGIKADVSLHCLHM 455
DB 421 HLLGMSCCLNPILYGLFNNGIKADVSLHCLHM 455

```

```

RESULT 2
ID NY5R_CANFA STANDARD; PRT; 446 AA.

```

```

AC 062729;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5
DE receptor) (NPY5).
GN NPYSR OR NPY5.
OS Canis familiaris (Dog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OK NCBI_TaxID=9613;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99017379; Pubmed=9802393;
RA Borowsky B., Walker M.W., Bard J., Weinschank R.L., Laz T.M.,
RA Vaysses P., Branchek T.A., Gerald C.
RT "Molecular biology and pharmacology of multiple NPY Y5 receptor
RT species homologs."
RL Regul. Pept. 75:45-53(1998).
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD
CC BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF049328; AAC17838.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 41 62 1 (POTENTIAL).
FT DOMAIN 63 74 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 75 95 2 (POTENTIAL).
FT DOMAIN 96 115 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 116 137 3 (POTENTIAL).
FT DOMAIN 138 157 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 158 178 4 (POTENTIAL).
FT DOMAIN 179 210 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 211 232 5 (POTENTIAL).
FT DOMAIN 233 311 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 311 391 6 (POTENTIAL).
FT DOMAIN 392 404 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 405 428 7 (POTENTIAL).
FT DOMAIN 429 446 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 114 198 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (POTENTIAL).
SQ SEQUENCE 446 AA; 51012 MW; 5CAB8D2CF5D254A CRC64;

```

```

Query Match 86.1%; Score 1581.5; DB 1; Length 446;
Best Local Similarity 71.7%; Pred. No. 1.3e-99;
Matches 319; Conservative 7; Mismatches 14; Indels 105; Gaps 3;
QY 11 MDLEDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLOLYFLGLGYTFVSLGFMGNL 70
DB 1 MDLEDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLOLYFLGLGYTFVSLGFMGNL 70
QY 71 LILALMAKRNQKTTVNFILGNLAFSDLLVLFCSPTFLTSVLDQWNGKVMCHIMFPL 130
DB 71 LILALMAKRNQKTTVNFILGNLAFSDLLVLFCSPTFLTSVLDQWNGKVMCHIMFPL 130

```

ID	NAME	STANDARD	PRT	456 AA.			
DB	61	LILMALMRKRNQKTMVNFNLGNLAFSDILVVLVCSPEPTLTLVLLDQMGKWC	120				
QY	131	OCVSVLSTLLISLAIYVRHMIKHPISNNLTAHGXYFLATVWLTGPAICSP	190				
DB	121	OCVSVLSTLLISLAIYVRHMIKHPISNNLTAHGXYFLATVWLTGPAICSP	180				
QY	191	VELQETPCSSALLSRVLCVSPSDSRIAPFTLSLLVQYILPLVCLTASHTS	245				
DB	181	VELQETPCSSALLSRVLCVSPSDSRIAPFTLSLLVQYILPLVCLTASHTS	240				
QY	246	-----IakRR-----	251				
DB	241	GLSKNKLEENEMINLTLOPFKSGQVQLSSSHKWSYFIKHKRRRSKKTAC	300				
QY	252	-----NNMKDKRDK--YRS	265				
DB	301	ARPEQENSRMLPENFGSVRSQSHSSSKFIPGVPTCEPKPEPNSDVHDM	360				
QY	266	SRSRSVFRRLLTLILVFAVSMPLHLFHHVYTDPRNDLISNRHKLYCIC	325				
DB	361	KRSRSVFRRLLTLILVFAVSMPLHLFHHVYTDPRNDLISNRHKLYCIC	420				
QY	326	NPIIXGFLNKGICADLVLSICLHM	350				
DB	421	NPIIXGFLNKGICADLVLSICLHM	445				
RESULT 3							
	NY5R_RAT						
ID	NY5R_RAT	STANDARD	PRT	456 AA.			
AC	063634	P70586					
DT	01-NOV-1997	(Rel. 35, Created)					
DT	01-NOV-1997	(Rel. 35, Last sequence update)					
DT	30-NOV-2000	(Rel. 39, Last annotation update)					
DE	Neuropeptide y receptor type 5 (NPY-5 (NPY-5 receptor) (Y5 receptor))						
GN	NPY5R OR NPYR5.						
OS	Rattus norvegicus (Rat).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
OX	NCBI_TaxID=10116						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Brain:						
RX	MEDLINE=96317589; PubMed=8700207;						
RA	Gerald C., Walker M.W., Cristione L., Gustafson E.L.,						
RA	Barzil-Hartman C., Smith K.E., Vaysse P., Durkin M.M., Laz T.M.,						
RA	Lillemeyer D.L., Schnafhauser A.O., Whitebread S., Hofbauer K.G.,						
RA	Taber K.I., Branchek T.A., Weinshank R.L.;						
RT	"A receptor subtype involved in neuropeptide-Y-induced food intake.";						
RL	Nature 383:168-171(1996).						
RN	[2]						
RP	SEQUENCE OF 12-456 FROM N.A.						
RC	TISSUE=Brain:						
RA	MEDLINE=96332165; PubMed=9669502;						
RA	Parker E.M., Babi J.C.K., Balasubramaniam A., Burrier R.E., Guzzi M.,						
RA	Hamm F., Mukhopadhyay G., Rudinski M.S., Tao Z., Tice M., Xia L.,						
RA	Mullins D.E., Salisbury B.G.;						
RT	"Gp231118 (1229991) and other analogues of the C-terminus of						
RT	neuropeptide Y are potent neuropeptide Y Y1 receptor antagonists and						
RT	neuropeptide Y Y4 receptor agonists.";						
RL	Eur. J. Pharmacol. 349:97-105(1998).						
RN	[3]						
RP	SEQUENCE OF 12-456 FROM N.A.						
RC	STRAIN=Sprague-Dawley:						
RX	MEDLINE=96421636; PubMed=8824284;						
RA	Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,						
RA	Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,						
RA	Sadlovski Y., Schaefer J., Velazquez N., McCabe M.L.;						
RT	"Identification of a novel hypothalamic neuropeptide Y receptor						
RT	associated with feeding behavior.";						
J. Biol. Chem.	271:26315-26319(1996).						
-1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY							

	CC	OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS.
	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
	CC	-I- TISSUE SPECIFICITY: BRAIN; HYPOTHALAMUS.
	CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO YACHKININS RECEPTORS.
	CC	-----
	CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-stb.ch/announce/">http://www.isb-stb.ch/announce/</a> or send an email to <a href="mailto:license@isb-stb.ch">license@isb-stb.ch</a> ).
	CC	-----
DR	EMBL:	U56078; AAC52677.1; .
DR	EMBL:	AFO44264; AAC15670.1; .
DR	EMBL:	U66274; AAC52845.1; .
DR	InterPro:	IPIR00276; GPCR_Rhodopsn.
DR	Pfam:	PF00001; 7tm_1; 1.
DR	PROSITE:	PS00237; G_PROTEIN_RECIP_FL_2; 1.
DR	PROSITE:	PS0262; G_PROTEIN_RECIP_FL_2; 1.
KM	G-protein coupled receptor; Transmembrane; Glycoprotein;	
KW	Phosphorylation; Lipoprotein; Palmitate.	
FT	DOMAIN	1 50 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	52 73 1 (POTENTIAL).
FT	DOMAIN	74 85 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	86 106 2 (POTENTIAL).
FT	DOMAIN	107 126 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	127 148 3 (POTENTIAL).
FT	DOMAIN	149 168 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	169 189 4 (POTENTIAL).
FT	DOMAIN	190 221 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	222 243 5 (POTENTIAL).
FT	DOMAIN	244 322 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	379 401 6 (POTENTIAL).
FT	DOMAIN	402 414 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	415 438 7 (POTENTIAL).
FT	DOMAIN	439 456 CYTOPLASMIC (POTENTIAL).
FT	DISULFID	125 209 BY SIMILARITY.
FT	LIPID	452 452 PALMITATE (POTENTIAL).
FT	CARBOHYD	21 21 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	28 28 N-LINKED (GLCNAG. . .) (POTENTIAL).
SQ	SEQUENCE	456 AA; 51715 MW; 5157ABE341BA707E CRC64;
	Query Match	83.7%; Score 1536; DB 1; Length 456;
	Best Local Similarity	67.9%; Pred. No. 8.2e-88;
	Matches 304; Conservative 21; Mismatches 19; Indels 104; Gaps 3;	
OY	7 GDYNDDLEDEYXNTLTATNTNTAATRNDSDFVMDYSKYVDLOYFLGLGYTPSLGFF	66
DB	8 QOSSSEPKLEEHNFTPTENTNTAAARNAPAFAMEDYKRSVDLOFPFLGLTYEVSLSGF	67
OY	67 MGNLLILMAAMKRNRQKTTFVNFLIGNLAESDIILVLFCSPTTLTSVLDDMMFGKVMCHI	126
DB	68 MGNLLILMAVMKKRRNQKTTNVNFIIGNLAESDIILVLFCSPTTLTVSLDDMMFGKVMCHI	127
OY	127 MFELQCVSVLSTLLISIAIVRYIMIKHPISNNLTANHGYFLIATVWTLGFAICSPLYV	186
DB	128 MFELQCVSVLSTLLISIAIVRYIMIKHPISNNLTANHGYFLIATVWTLGFAICSPLYV	187
OY	187 FHSIVELOETFSALLSSRYLCVESMPSPSYRTAFITISLLVOYLPLVCLVSHPTSC-	245
DB	188 FHSIVELETFESSALLSKYLCVESMPSPSYRTAFITISLLVOYLPLVCLVSHPTSCVR	247
OY	246 ---IRLKRRNNMDK-----MRDNKYRSS-----	266
DB	248 SISGLSHKENLEENEMINLTGPSKKSRNQAKTPPTQKMYSITRKHHRRYSKTKACY	307
OY	267 -----	266
DB	308 LPAPGPSOGKHAVPENPASVRSQSPPSKVIPGVPCIFCEVKPESSDAHEMRVKSIT	367

QY 267 ----RSRSVFRLLTLLVFAVSWMPHLFHVYDFDNDNLISNRHFLVYCICHLGMS 322  
 DB 368 RIKRSRSVFRLLTLLVFAVSWMPHLFHVYDFDNDNLISNRHFLVYCICHLGMS 427  
 QY 323 CCLNPILYGLFNLNGIKADLVSLHCLHM 350  
 DB 428 CCLNPILYGLFNLNGIKADLVSLHCLHM 455

RESULT 4  
 NY5R\_PIG STANDARD; PRT; 446 AA.  
 AC 097969;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5 receptor)  
 GN NPY5R OR NPYR5.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wraith A., Torsten A., Chardon P., Harbitz I., Chowdhary B.P., Andersson L., Larhammar D., Porcine NPY receptors NPY1R, NPY2R and NPY5R: cloning, mapping and comparative analysis";  
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=LMD; TISSUE=Kidney;  
 RA Ito Y., Minezawa M.;  
 RT "Sus scrofa gene for neuropeptide Y receptor type 5, complete cds.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO TACHYKININS RECEPTORS.  
 CC -----  
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AF106083; AAD13778.1; -  
 DR EMBL: AB019185; BA34055.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsin.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; FALSE\_NEG.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 39  
 FT TRANSMEM 41 62  
 FT DOMAIN 63 74  
 FT TRANSMEM 75 95  
 FT DOMAIN 96 115  
 FT TRANSMEM 116 137  
 FT DOMAIN 138 157  
 FT TRANSMEM 158 178  
 FT DOMAIN 179 210  
 FT TRANSMEM 211 232  
 FT DOMAIN 233 311

FT TRANSMEM 369 391 6 (POTENTIAL).  
 FT DOMAIN 392 404 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 405 428 7 (POTENTIAL).  
 FT DOMAIN 429 446 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 114 198 BY SIMILARITY.  
 FT LIPID 442 442 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50474 MW; B7F616C2394C6CA0 CRC64;

Query Match 83.6%; Score 1534.5; DB 1; Length 446;  
 Best Local Similarity 68.8%; Pred. No. 9.9e-88;  
 Matches 306; Conservative 17; Mismatches 17; Indels 105; Gaps 3;

QY 11 MDLEDEYYNKTATENNNTATRNSDPPVWDYKSSVDDLOFLIGLYTEVSLGFGMNL 70  
 DB 1 MGSLEIPYXNKTATSENNTATRNSGPFWEDYKGSVDDLOFLIGLYTEVSLGFGMNL 60  
 QY 71 LILMAKKRRNQKTYVNFIGNLAFSDILVLFCSPTFTSVLLDQWMEGKVMCHIMPTL 130  
 DB 61 LILMAVRRKRNQKTYVNFIGNLAFSDILVLFCSPTFTSVLLDQWMEGKVMCHIMPTL 120  
 QY 131 QCVSVLVSTLLISIAIVRYHMKHPSNNITANHGFLATVWTGLFATCSPLPVRHSL 190  
 DB 121 QCVTVLVSTLLISIAIVRYHMKHPSNNITANHGFLATVWTGLFATCSPLPVRHSL 180  
 QY 191 VELQETFGSALLSRVLCVESPDSYRIAFITSLLVQYTLPLVCLTVSHTSVC----- 245  
 DB 181 VELQETFGSALLSRVLCVESPDSYRIAFITSLLVQYTLPLVCLTVSHTSVCRIATSC 240  
 QY 246 -----IRLKR----- 251  
 DB 241 GLSSQDSKLEENEMINLTLPKRRSGPQAKLSHPKWTYSFIRRRRYSKTCACVPAP 300  
 QY 252 -----NNMDKRRDNK-----YRS 265  
 DB 301 AGPLERREGRPPKVGSMOSQPPPSKFMPCVTCPEVKRENSDVPEKMSISIRLR 360  
 QY 266 SRSRSVFRLLTLLVFAVSWMPHLFHVYDFDNDNLISNRHFLVYCICHLGMS 325  
 DB 361 KRSSRSVFRLLTLLVFAVSWMPHLFHVYDFDNDNLISNRHFLVYCICHLGMS 420  
 QY 326 NPILYGLFNLNGIKADLVSLHCLHM 350  
 DB 421 NPILYGLFNLNGIKADLVSLHCLHM 445

RESULT 5  
 NY5R\_MOUSE STANDARD; PRT; 466 AA.  
 ID NY5R\_MOUSE  
 AC 070342; O35380; Q9JMK1;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5 receptor)  
 GN NPY5R OR NPY5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99017379; PubMed=9802393;  
 RA Borowsky B., Walker M.W., Bard J., Weinschenk R.L., Laz T.M., Vayssie P., Branchek T.A., Gerald C.;  
 RT "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs";  
 RL Regul. Pept. 75:45-53(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV; TISSUE=Brain;  
 RA Chen H., Adams S., McWhinnie E., Bayne M., Gadsby R., Zastawny R.;



"Mouse neuropeptide Y Y5 receptor characterized by repeat sequence in extracellular domain.";  
Submitted (Sep-1997) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
RX MEDLINE-97459646; PubMed-9315606;  
RA Nakamura M., Yokoyama M., Watanabe H., Matsunoto T.;  
RT "Molecular cloning, organization and localization of the gene for the mouse neuropeptide Y-Y5 receptor.";  
RL Biochem. Biophys. Acta 1328:83-89(1997).  
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEKS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: AF049329; AAC17839.1; -  
DR EMBL: AF022948; AAB81829.1; -  
DR EMBL: AB001346; BAA89538.1; -  
DR MGI:108082; Npy5r.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G-PROTEIN-RECEP\_FL1; FALSE\_NEG.  
DR PROSITE: PS50262; G-PROTEIN-RECEP\_FL2; 1.  
KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
KM Phosphorylation; Lipoprotein; Palmitate.  
FT DOMAIN 11 60  
TRANSMEM 62 83  
FT DOMAIN 84 95  
TRANSMEM 96 116  
FT DOMAIN 117 136  
TRANSMEM 137 158  
FT DOMAIN 159 178  
TRANSMEM 179 199  
FT DOMAIN 200 231  
TRANSMEM 232 253  
FT DOMAIN 254 332  
TRANSMEM 389 411  
FT DOMAIN 412 424  
TRANSMEM 425 448  
FT DOMAIN 449 466  
TRANSMEM 467 484  
FT DISULFID 135 219  
LIPID 462 462  
FT CARBOHYD 10 10  
CARBOHYD 17 17  
FT CARBOHYD 38 38  
CARBOHYD 39 39  
FT CARBOHYD 195 195  
CONFLICT 284 284  
FT CONFLICT 284 284  
SO SEQUENCE 466 AA; 52784 MW; B157F236EFD4385 CRC64;  
  
Query Match 82.5%; Score 1514.5; DB 1; Length 466;  
Best local Similarity 65.6%; Pred. No. 1.7e-86;  
Matches 305; Conservative 19; Mismatches 16; Indels 125; Gaps 5;  
  
QY 11 MDLEDEYIKTLATENTAT-----RNSDPYWDYKSSVD 49  
Db 1 MEVLEHEFKRTVTEENTAAASONTASPAWEDYRGTEENTSAARNFAFPWEDYRGSVDD 60  
  
QY 50 LQYFLGLTFFVSLGFMGLILIMLMKKRQKTYNFIIGNLAFSDILVLFCSFTL 109  
Db 61 LQYFLGLTFFVSLGFMGLILIMLMKKRQKTYNFIIGNLAFSDILVLFCSFTL 120

QY 110 TSVLLDQMFQKWCMTPLQCVSLVSLIISIAIVRYHMKIPISNNLTANHCYFL 169  
Db 121 TSVLLDQMFQKWCMTPLQCVSLVSLIISIAIVRYHMKIPISNNLTANHCYFL 180  
  
QY 170 IATVMTLGFALICSPLPYFHSVLVLEQTFEGSALLSRKLCYESNPSDYSYIAFTISLLVQ 229  
Db 181 IATVMTLGFALICSPLPYFHSVLVLEQTFEGSALLSRKLCYESNPSDYSYIAFTISLLVQ 240  
  
QY 230 YIIPVLCVTSHTSVC-----IRLKRNNMD-----KMRD----- 260  
Db 241 YIIPVLCVTSHTSVCNCSISGSLSHKRNLENDMNLTHPSKSSDQAKPSTQKMSY 300  
  
QY 261 ---NRYR----- 264  
Db 301 SFIRKRRRYSKKTACVLPAPAGPSQEKHLTPENPGSVRSQSPSKVIGVPICFEVK 360  
  
QY 265 -----SSRSRYRTILILVAVSMPLHLFHYVTDRNDNLISN 305  
Db 361 PESSDAQENRVRKSLTRIKRRRSRYRTILILVAVSMPLHLFHYVTDRNDNLISN 420  
  
QY 306 RHFKLVYCIHLLGMSCNLPILYGLNNGIKADVLSTHCLHM 350  
Db 421 RHFKLVYCIHLLGMSCNLPILYGLNNGIKADVLSTHCLHM 465  
  
RESULT 6  
NYIR\_CANFA STANDARD; PRT; 382 AA.  
ID NYIR\_CANFA  
AC 002813;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Neuropeptide Y receptor type 1 (Npy1-R).  
GN NYIR.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RX MEDLINE-99017380; PubMed-9802394;  
RA Malmstrom R.E., Hoekfelt T., Bjorkman J.-A., Nihlen C., Bystrom M., Ekstrand A.J., Lundberg J.M.;  
RT "Characterization and molecular cloning of vascular neuropeptide Y receptor subtypes in pig and dog.";  
RL Regul. Pept. 75:55-70(1998)  
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: AF005778; AAC08046.1; -  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G-PROTEIN-RECEP\_FL1; 1.  
DR PROSITE: PS50262; G-PROTEIN-RECEP\_FL2; 1.  
KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
KM Phosphorylation; Lipoprotein; Palmitate.  
FT DOMAIN 1 38  
TRANSMEM 39 61  
FT DOMAIN 62 71  
TRANSMEM 72 93  
FT DOMAIN 94 113  
EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	114	135	3 (POTENTIAL)
FT <th>DOMAIN</th> <th>116</th> <th>155</th> <th>CYTOPLASMIC (POTENTIAL)</th>	DOMAIN	116	155	CYTOPLASMIC (POTENTIAL)
FT <th>TRANSMEM</th> <th>156</th> <th>176</th> <th>4 (POTENTIAL)</th>	TRANSMEM	156	176	4 (POTENTIAL)
FT <th>DOMAIN</th> <th>177</th> <th>209</th> <th>EXTRACELLULAR (POTENTIAL)</th>	DOMAIN	177	209	EXTRACELLULAR (POTENTIAL)
FT <th>TRANSMEM</th> <th>210</th> <th>231</th> <th>5 (POTENTIAL)</th>	TRANSMEM	210	231	5 (POTENTIAL)
FT <th>DOMAIN</th> <th>232</th> <th>262</th> <th>CYTOPLASMIC (POTENTIAL)</th>	DOMAIN	232	262	CYTOPLASMIC (POTENTIAL)
FT <th>TRANSMEM</th> <th>263</th> <th>285</th> <th>6 (POTENTIAL)</th>	TRANSMEM	263	285	6 (POTENTIAL)
FT <th>DOMAIN</th> <th>286</th> <th>298</th> <th>EXTRACELLULAR (POTENTIAL)</th>	DOMAIN	286	298	EXTRACELLULAR (POTENTIAL)
FT <th>TRANSMEM</th> <th>299</th> <th>322</th> <th>7 (POTENTIAL)</th>	TRANSMEM	299	322	7 (POTENTIAL)
FT <th>DOMAIN</th> <th>323</th> <th>382</th> <th>CYTOPLASMIC (POTENTIAL)</th>	DOMAIN	323	382	CYTOPLASMIC (POTENTIAL)
FT <th>CARBOHYD</th> <th>2</th> <th>2</th> <th>N-LINKED (GLCNAC. . .) (POTENTIAL)</th>	CARBOHYD	2	2	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT <th>CARBOHYD</th> <th>11</th> <th>11</th> <th>N-LINKED (GLCNAC. . .) (POTENTIAL)</th>	CARBOHYD	11	11	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT <th>CARBOHYD</th> <th>17</th> <th>17</th> <th>N-LINKED (GLCNAC. . .) (POTENTIAL)</th>	CARBOHYD	17	17	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT <th>CARBOHYD</th> <th>185</th> <th>185</th> <th>N-LINKED (GLCNAC. . .) (POTENTIAL)</th>	CARBOHYD	185	185	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT <th>DISULFID</th> <th>112</th> <th>197</th> <th>BY SIMILARITY</th>	DISULFID	112	197	BY SIMILARITY
FT <th>LIPID</th> <th>337</th> <th>337</th> <th>PAINTATE (POTENTIAL)</th>	LIPID	337	337	PAINTATE (POTENTIAL)
SO <th>SEQUENCE</th> <th>382 AA:</th> <th>44245 MW; 95B57D20D6299803 CRC64;</th> <th></th>	SEQUENCE	382 AA:	44245 MW; 95B57D20D6299803 CRC64;	
Query Match				
Best Local Similarity		35.4%;	Score 650;	DB 1; Length 382;
Matches 127; Conservative		40.4%;	Pred. No. 1.6e-33;	
		64;	Mismatches 117;	Indels 6; Gaps 3
QY	32	TRANSPEPTWDDKSSVDLDQYFLIGL-YTFVSLDGFMGHLLMALMKRKNQKTYVNFIL	90	
DB	19	SENSQFLAFESDDCHLPLAMIFTLALAGCAVILIGTGALIMILKKEKERNVTNII	78	
QY	91	GNIAFSDLIVFCSPFTLTSVLLDQMGKWCACHMPLOCVSVLSTLLISIAIVRY	150	
DB	79	VNLSSDILVALMCLPFTFVTYTLMDHWGEMKCKLNPVQCVSTVTSFSLVILAVENH	138	
QY	151	HMKHPISNNLTANHGYELLATVWTGLFAICSPLPVFSHSLVLEDTFGSALLSS--RYL	207	
DB	139	QLILRCWRPNRPNHAYVGIAYIVWL--AVVSSLPFLIQLYVLTDEPFOVNTLDAEKDKYV	196	
QY	208	CYESMPSSDYRIAPFISLLVYLIVLCIATVSHTSVCIRLKRNNMMDKMDNXYRSSR	267	
DB	197	CFDKPSSDHRSLSTLLMLDQYFSPLCIFICYKRYIIRLKRNNMMDKMDNXYRSSR	256	
QY	268	SRSVYFRLTLILVAVSMPLRFLHFVYTDENDNISNHRFLVYCICHLGLMMSCLLNP	327	
DB	257	TKRINIMLSIVAVRVCMLPLTINFYFDWMHQIILACNHNLLPLCLGLTAMISTCVNP	316	
QY	328	ILYGLNNGIKADL	341	
DB	317	IFYGLNKNFORDL	330	
RESULT 7				
NYIR_PIG				
ID	NYIR_PIG	STANDARD:	PRT:	383 AA.
AC	002835;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Neuropeptide y receptor type 1 (NPY1-R).			
GN	NPY1R.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID:9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hypothalamus;			
RX	MEDLINE=99017380; PubMed=9802394;			
RA	Malmsstrom R.E., Hoekfelt T., Bloerkmann J.-A., Bystroem M.,			
RA	Ekstrand A.-J., Lundberg J.M.,			
RT	"Characterization and molecular cloning of vascular neuropeptide y			
RT	receptor subtypes in pig and dog."			
RL	Regul. Pept. 75:55-70(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Wraith A., Tornsten A., Chardon P., Harditz I., Chowdhary B.P.,			
RA	Andersson L., Larhammar D.;			

RT	"Porcine NPY receptors, NP1YR, NP2YR and NP15R: Cloning, mapping and comparative analysis.";	
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.	
CC	- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.	
CC	- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
CC	HIGHEST TO "ACHKININS RECEPTORS."	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL:	AF005779; AAC26836.1; -
DR	EMBL:	AF106081; AAD33776.2; -
DR	InterPro:	IPR000276; GPCR_Rhodopsn.
DR	Pfam:	PF00001; 7tm_1; 1.
DR	PRINTS:	PR00237; GPCRHHODOPSN.
DR	PROSITE:	PS00237; G-PROTEIN_REC_P1_1; 1.
DR	PROSITE:	PS50262; G-PROTEIN_REC_P1_2; 1.
KM	G-protein coupled receptor; Transmembrane; Glycoprotein;	
KV	Phosphorylation; Lipoprotein; Palmitate.	
FT	DOMAIN	1 39
FT	TRANSMEM	40 62
FT	DOMAIN	63 72
FT	TRANSMEM	73 94
FT	DOMAIN	95 114
FT	TRANSMEM	115 136
FT	DOMAIN	137 156
FT	TRANSMEM	157 177
FT	DOMAIN	178 210
FT	TRANSMEM	211 232
FT	DOMAIN	233 263
FT	TRANSMEM	264 286
FT	DOMAIN	287 299
FT	TRANSMEM	300 323
FT	DOMAIN	324 383
FT	CARBOHD	2 2
FT	CARBOHD	11 11
FT	CARBOHD	17 17
FT	DISULFD	113 198
FT	LIPID	338 338
FT	CONFLICT	203 203
FT	SEQUENCE	383 AA; 44327 MW; 0D58CBCA549B62CF CMC64;
QY	Query Match	35.4%; Score 650; DB 1; Length 383;
QY	Best Local Similarity	39.3%; Pred. Misat. 1.6e-33;
QY	Matches 129; Conservative	68; Mismatches 116; Indels 15; Gaps 4;
DB	18 YUNKPLATEENMTAARNSDPVMDDYKSSVDDLYQVELGL- YTPVSLGFGPNNLLMAL	76
DB	15 YYN-----FSKSNQFLAFENDCHPLAMETFLATLAVGAATILGVSGNLLALIIIT	65
QY	77 MKRNRQKTTVEFLIGNLAFSDILVVLFCSPFTLLSVLLDDMMFGKVMCHINPFLQCVSVL	136
DB	66 LKQKMRVNTVILILVNSFSDLVAIMCLPFTFYVTLMDHNVFGEVGMKLNPFVQCVSIT	125
QY	137 VSTLILSIAIVRHMIMKHPISNNLTANHGVELATVWTLGFAICSPLPVFNLSLVEOET	196
DB	126 VSIETSLVIAVERHOLLINPRGWRPSNRHAAVLAIVWL--AASSSPFLIYOVLDEP	183
QY	197 FGSALLS---RYLCVESMPSDSYRIATLISLLLVQYLPLVCLVTSVSCIRLKRNN	253
DB	184 FQWNTLDFKQKYCEDFSLSDSHSLSTYLLVLVQYFGPLCFITCYEKKYIRLKRNN	243
QY	254 MMDKMRDKYRSRSRSVFYRLLILVFAVSMPLRLEFHVVTQENDNLISNRHFLYVC	313
DB	244 MMDKMRDKYRSSEKRRKNVWLLSIVAFVNCWPLRTITFNIVPDMNDIATCNHNLFL	303
QY	314 ICHLLGMWSCCLNPLILYGLFNNGIKADI	341

```

Db 304 LCHLTAMISTCINPIFYGLNKNFORDL 331
      :||| :|:|:| :||| :||| :|||
RESULT 8
NYIR_HUMAN STANDARD; PRT; 384 AA.
ID NYIR_HUMAN
AC P25929;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 1 (NPY1-R).
GN NPY1R OR NPYR OR NPY1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92283782; PubMed=1317848;
RA Larhammar D., Blomqvist A.G., Yee F., Jazin E.E., Yoo H.,
RA Mahlestedt C.R.;
RT 'Cloning and functional expression of a human neuropeptide Y/peptide
RT Y receptor of the Y1 type.';
RL J. Biol. Chem. 267:10935-10938(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92335184; PubMed=1321422;
RA Herzog H., Hort Y.J., Ball H.J., Hayes G., Shine J., Selbie L.A.;
RT 'Cloned human neuropeptide Y receptor couples to two different second
RT messenger systems.';
RL Proc. Natl. Acad. Sci. U.S.A. 89:5794-5798(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93203272; PubMed=8095935;
RA Herzog H., Baumgartner M., Vivero C., Selbie L.A., Auer B., Shine J.;
RT 'Genomic organization, localization, and allelic differences in the
RT gene for the human neuropeptide Y Y1 receptor.';
RL J. Biol. Chem. 268:6703-6707(1993).
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK
CC ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES IS
CC NPY > [PRO-34] PYY, PYY AND [LEU-31, PRO-34] NPY > NPY (2-36) >
CC [ILE-31, GLN-34] PP AND PYY (3-36) > PP > NPY FREE ACID.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: M8461; AAA73215.1; -
DR EMBL: M84755; AAA59920.1; -
DR EMBL: L07614; -; NOT_ANNOTATED.CDS.
DR EMBL: L07615; AAA59947.1; -
DR EMBL: A26481; CAA01819.1; -
DR EMBL: A26126; CAA01787.1; -
DR PIR: A42773; A42773.
DR PIR: A46133; A46133.
DR PIR: A45490; A45490.
DR Genew; HGNC:7956; NPY1R.
DR MIM: 162641; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR000237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.

```

```

DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 39
FT TRANSSEM 40 62
FT DOMAIN 63 72
FT TRANSSEM 73 94
FT DOMAIN 95 114
FT TRANSSEM 115 136
FT DOMAIN 137 156
FT TRANSSEM 157 177
FT DOMAIN 178 210
FT TRANSSEM 211 232
FT DOMAIN 233 263
FT TRANSSEM 264 286
FT DOMAIN 287 299
FT TRANSSEM 300 323
FT DOMAIN 324 384
FT CARBOHYD 2
FT CARBOHYD 11 11
FT CARBOHYD 17 17
FT DISULFID 113 198
FT LIPID 338 338
FT CONFLICT 96 96
FT SEQUENCE 384 AA; 44392 MW; 582B0DB04490316 CRC64;

Query Match 35.1%; Score 644; DB 1; Length 384;
Best Local Similarity 37.9%; Pred. No. 3.8e-33;
Matches 130; Conservative 70; Mismatches 122; Indels 21; Gaps 5;

QY 3 FYSKODYNMDELDEYNYKTLATENNNTAATRNDSFPPWDYKSSVDDLOYFLGL- YTFV 61
Db 6 FSYQENHSVSHNSFSEKNAQLAFEND-----DCHLPL-----AMFTLALAGAV 50
QY 62 SLGFGNLLILMALAKKRKKQKTTVNFILGNLAFSDILVYLFCSPTFLTVLDDQNMFGK 121
Db 51 IILGVSGNLLILILKQKEMRNVNTILIVNLSFSDILVIMCPFFVYVYTLMDHWGFE 110
QY 122 VMCHIMPELOCVSVLTVLILISIAIVRYMHKIPISNNLTANNGYGLIATVMTLGAFC 181
Db 111 AMCKLNFVOCVSTIVTSFSLVLAVERHQLITPKGRNRRNHAYGVIAVIVYL--AVA 168
QY 182 SPLPVFSLVLEQETFGSALLSS---RYLCVESNPDSYRIAFITSLLYOYTLPLVCLT 238
Db 169 SSLPFLYQWMTDEPFQNVFLDAKDYKCFDQPSDSHRLSTYTLVLVQYGPCLCFIF 228
QY 239 VSHRTSVIRLAKRRNMMDKKRDKKYSRSRSVYRLLTILVFAVSMPLHLFHYVTD 298
Db 229 ICYFKYIRLKRNRNMMDKKRDKKYSRSSETRKINIMLSIVAFVACWMLPTITFVFDW 288
QY 299 NDNLISNRHFKLVYCIHLGMMSSCCNPILYGLNNGIRADL 341
Db 289 NHOIATCINNLLFLCHLTAMISTCVNPIFYGLNKNFORDL 331

RESULT 9
NYIR_CAVPO STANDARD; PRT; 383 AA.
ID NYIR_CAVPO
AC Q9WUD0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 1 (NPY1-R).
GN NPY1R.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99427767; PubMed=10499421;
RX Berglund M.M., Holmberg S.K.S., Eriksson H., Gedda K., Mafstrand J.-P.,
RX Serradell-Le Gal C., Chhajlani V., Grundemar L., Larhammar D.;

```

```
RT "The cloned guinea pig neuropeptide Y receptor Y1 conforms to other
RT mammalian Y1 receptors."
RL Reptides 20:1043-1053(1999).
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: AF135061; AAD43060.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 40 62 1 (POTENTIAL).
FT TRANSSEM 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 73 94 2 (POTENTIAL).
FT TRANSSEM 95 114 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 115 136 3 (POTENTIAL).
FT TRANSSEM 137 156 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 157 177 4 (POTENTIAL).
FT TRANSSEM 178 210 5 (POTENTIAL).
FT TRANSSEM 211 232 6 (POTENTIAL).
FT TRANSSEM 233 263 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 264 286 6 (POTENTIAL).
FT TRANSSEM 287 299 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 300 323 7 (POTENTIAL).
FT TRANSSEM 324 383 7 (POTENTIAL).
FT CARBOHYD 2 2 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 113 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 338 338 BY SIMILARITY.
SQ SEQUENCE 383 AA; 44281 MW; E53BD93FAV35FE8 CRC64;

Query Match 34.9%; Score 640.5; DB 1; Length 383;
Best Local Similarity 37.8%; Pred. No. 6,2e-33;
Matches 130; Conservative 70; Mismatches 123; Indels 21; Gaps 5;

QY 2 SFPSKQDYNDLEDEYNNKTATENNNTATRNSDFPVMDYKSSVDDLYQFLGL-VTF 60
DB 5 SFQLEHNSHYNNLSEKPSFEAFEND-----DCHLP-----AVFTLALAYGA 49
QY 61 VSLGFGNLLIIMALKRRKNOKTTVNFELGNLAFSDILVLFCSPTLISVLLDDMMFG 120
DB 50 VIIIGVGNLALILIIKKQEMRNVNIIILVNSFSDILVIMKLPETFYVTLMDHWIFG 109
QY 121 KVMCHNMPFLQCVSVLTLISIAIVRYHMKIPISNNLTANHGFLATVTLGFAI 180
DB 110 EIMCKLMPFQCVSIVISFSLVLAVERHQLLINPRGWRNNHAIIGIAVIVL--AV 167
QY 181 CSPLPVHSHLVEQETGSAALLS--RYLCVESWPSDSRIATFTLLVQYTLPLVC 237
DB 168 ASSLPFMYIVLDEPQNTVLDLAFKDKLVCFQDPSPDSHRLSYTLLVLYQYGFCEI 227
QY 238 TVSHTSVCILKRRNNMMDKRRKSSRSRYFRLTLLILVFNASWMPDHFHVTD 297
DB 228 FICYFYIYILKRRNNMMDKRRKSSRSRYFRLTLLILVFNASWMPDHFHVTD 287
QY 298 FNDNLISNRHFKLVYCCILHGLGMMSCCLNPLILYGLNNGIKADL 341
DB 288 WNHQIATACNHNLLFLCHLTAMISTCVNPIFGFLKNKFORDL 331
```

```
RESULT 10
NR1_XENLA STANDARD; PRT; 366 AA.
AC P34992;
ID 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE Neuropeptide Y receptor type 1 (NPY-R).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N. A.
RC Tissue-Hypothalamus;
RA Mattens G.J.M., Blomqvist A.G., Roubos E.W., Larhammar D.;
RL Submitted (xxx-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: L25416; AAA49918.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 35 57 1 (POTENTIAL).
FT TRANSSEM 58 67 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 68 89 2 (POTENTIAL).
FT TRANSSEM 90 109 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 110 131 3 (POTENTIAL).
FT TRANSSEM 132 151 4 (POTENTIAL).
FT TRANSSEM 152 172 5 (POTENTIAL).
FT TRANSSEM 173 205 6 (POTENTIAL).
FT TRANSSEM 206 227 7 (POTENTIAL).
FT TRANSSEM 228 258 8 (POTENTIAL).
FT TRANSSEM 259 281 9 (POTENTIAL).
FT TRANSSEM 282 294 10 (POTENTIAL).
FT TRANSSEM 295 318 11 (POTENTIAL).
FT TRANSSEM 319 366 12 (POTENTIAL).
FT CARBOHYD 2 2 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 108 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 333 333 BY SIMILARITY.
SQ SEQUENCE 366 AA; 42252 MW; B82C3C19A603FC67 CRC64;

Query Match 34.7%; Score 637; DB 1; Length 366;
Best Local Similarity 38.5%; Pred. No. 9,8e-33;
Matches 126; Conservative 71; Mismatches 120; Indels 10; Gaps 5;

QY 19 YNKLATENNNTATRNSDFPVMDYKSSVDDLYQFLGL-VTFVSLGFGNLLIIMALK 77
DB 6 YFENLSVPNNISG--NTTFPISDCALPLP--MIFTLALYGAIVIIIGLSGNLALIIII 61
QY 78 KRRNQKTTVNFELGNLAFSDILVLFCSPTLISVLLDDMMFGKVMCHNMPFLQCVSV 137
```

```

DB      62 KQEMRVNITLVNLSFSDLATIMCLPPTLLYTLMDHIFGEVWCKLMEYIQCVSVTV 121
      138 STILISIAIVRYHMIKHPISNNLTANHGFLIATVATLGFALICSPLPVPHSIVELOETF 197
      122 SITSVLIAIERHQLIINPRGMRPNRHACFGITVINGFMACTPLMAMSVLTD--EPF 179
      198 GSALLSS---RYLCVESWPSDSYRIAFITSLLYOYILPLVCLTVSHTSVCIRLKRNNM 254
      180 KNISLDSYIGKYVCLDEDFEDKFRLSYSTLLFLITQYLGCLFEVCYTKIFLRKRNNM 239
      255 MDMKRNKRRSSRSRSVRYTLTILLVFANSMPLHFLHYVTPDNLIINRPFKYCYC 314
      240 MDKIRNKRSSSETKRINIMLSIVGFALCMLPFFIFNLVPMNBEAVATCNHNLFLI 299
      315 CHLLGMSCCLNPILYGLFNLNGIKADL 341
      300 CHLTAMISTCVNPFIYGFGLNKNFORDL 326

RESULT 11
NYIR.MOUSE
ID      NYIR.MOUSE      STANDARD:      PRT:      382 AA.
AC      004573; 061993;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Neuropeptide Y receptor type 1 (NPY1-R).
GN      NPY1R.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      TISSUE=Liver;
RX      MEDLINE=93106169; PubMed=1468559;
RA      Eva C., Oberto A., Sprengel R., Genazzani E.;
RT      "The murine NPY-1 receptor gene. Structure and delineation of tissue-
RT      specific expression.";
RL      FEBS Lett. 314:285-288(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96102072; PubMed=8530415;
RA      Nakamura M., Sakana C., Aoki Y., Ogasawara H., Tsuji T.,
RA      Kodama H., Matsumoto T., Shimizu T., Noma M.;
RT      "Identification of two isoforms of mouse neuropeptide Y-Y1 receptor
RT      generated by alternative splicing. Isolation, genomic structure, and
RT      functional expression of the receptors.";
RL      J. Biol. Chem. 270:30102-30110(1995).
CC      -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: NPY1-R ALPHA (SHOWN HERE) AND
CC      NPY1-R BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: THE ALPHA FORM IS HIGHLY EXPRESSED IN THE
CC      BRAIN, HEART, KIDNEY, SPLEEN, SKELETAL MUSCLE, AND LUNG, WHEREAS
CC      THE BETA RECEPTOR MRNA WAS NOT DETECTED IN THESE TISSUES. HOWEVER,
CC      THE BETA FORM IS EXPRESSED IN MOUSE EMBRYONIC DEVELOPMENTAL STAGE
CC      (7 AND 11 DAYS), BONE MARROW CELLS AND SEVERAL HEMATOPOIETIC CELL
CC      LINES.
CC      -1- DEVELOPMENTAL STAGE: THE BETA FORM IS EXPRESSED IN EMBRYONIC
CC      DEVELOPMENTAL STAGE (7 AND 11 DAYS). THE BETA FORM IS AN EMBRYONIC
CC      AND A BONE MARROW FORM OF NPY1-R, WHICH DECREASES IN THE
CC      EXPRESSION DURING DEVELOPMENT AND DIFFERENTIATION.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      HIGHEST TO TACHYKININS RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

```

CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: 218280; CAA79157.1; -.
CC      DR      EMBL: 218281; -. NOT ANNOTATED_CDS.
CC      DR      EMBL: D63818; BAA09887.1; -.
CC      DR      EMBL: D63819; BAA09888.1; -.
CC      DR      PIR: S27388; S27388.
CC      DR      MGD: MG1:104963; NPY1r.
CC      DR      InterPro: IPR000276; GPCR_Rhodopsin.
CC      DR      Pfam: PF00001; 7tm.1; 1.
CC      DR      PRINTS: PR00237; GPCRHHODOPSIN.
CC      DR      PROSITE: PS00237; G_PROTEIN_RECEP_F1_1.
CC      DR      PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC      KW      G-protein coupled receptor; Transmembrane; glycoprotein;
CC      KW      phosphorylation; Lipoprotein; Palmitate; Alternative splicing.
CC      FT      DOMAIN 1
CC      FT      TRANSMEM 39..61
CC      FT      DOMAIN 2
CC      FT      TRANSMEM 62..71
CC      FT      TRANSMEM 72..93
CC      FT      DOMAIN 3
CC      FT      TRANSMEM 94..113
CC      FT      TRANSMEM 114..135
CC      FT      TRANSMEM 136..155
CC      FT      TRANSMEM 156..176
CC      FT      TRANSMEM 177..209
CC      FT      TRANSMEM 210..231
CC      FT      TRANSMEM 232..262
CC      FT      TRANSMEM 263..285
CC      FT      TRANSMEM 286..298
CC      FT      TRANSMEM 299..322
CC      FT      DOMAIN 3
CC      FT      TRANSMEM 323..382
CC      FT      CARBOHYD 2
CC      FT      CARBOHYD 11
CC      FT      CARBOHYD 17
CC      FT      CARBOHYD 112
CC      FT      DISULFID 112..197
CC      FT      LIPID 337..337
CC      FT      VARSPIC 304
CC      FT      VARSPIC 308
CC      FT      VARSPIC 382
CC      SQ      SEQUENCE 382 AA; 44014 MW; CDCCF93E3ABABD70 CRC64;

Query Match          34.5%; Score 633.5; DB 1; Length 382;
Best local Similarity 37.8%; Pred. No. 1,7e-32;
Matches 127; Conservative 73; Mismatches 115; Indels 21; Gaps 6;

      20 NKTLL--ATENNNTA--ATRNSDPEVWDYKSSVDLQYFLIGLYTF-----VSLGLFMG 68
      2 NSTLFSVEVHSHIYNASENSPLAFEN-----DDCHLPLAVIFTLALAVAGVILIGVSG 56
      69 NLILALMKRRKQKTVNFLIGNLAFSDILVLFCSPTFLTSVLLDQMGKVMCHIMP 128
      57 NLALIIILKQKEMRVNITLVNLSFSDLVAVMCLPFFVYVYTLMDHWFGEFMCKLNP 116
      129 FLOCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVATLGFALICSPLPVPH 188
      117 FVOCVSTVTSVLSVLAVLVERHQLINPRGMRPNRHAIIGITVIVLAVASSLPEVITY 176
      189 SVELOETFGSALLSS---RYLCVESWPSDSYRIAFITSLLYOYILPLVCLTVSHTSVC 245
      177 ILND--EPFNVSIAFKDKVYVCDKRPDSHRSYSTLLVLIVGEPRLCFIFCYKIV 234
      246 IRLKRRNNMDKMRNDKRRSSRSVRYTLTILLVFANSMPLHFLHYVTPDNLIINRPFKY 305
      235 IRLKRRNNMDKIRDSYRSSETKRINIMLSIVGFALCMLPFFIFNLVPMNBEAVATCNH 294
      306 RHFKLYVCIHLLGMSCCLNPILYGLFNLNGIKADL 341
      295 CNHNLFLFCHLTAMISTCVNPFIYGFGLNKNFORDL 330

RESULT 12
NYIR.RAT
ID      NYIR.RAT      STANDARD:      PRT:      382 AA.
AC      P21555;
DT      01-MAY-1991 (Rel. 18, Created)

```

DT 01-MAY-1992 (Rel. 22, last sequence update)  
 DT 30-MAY-2000 (Rel. 39, last annotation update)  
 DE Neuropeptide Y receptor type 1 (NPY1-R) (FC5).  
 GN NPY1R.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=91032093; PubMed=2172008;  
 RA Eva C., Keisänen K., Mønyer H., Seeburg P.H., Sprengel R.;  
 RT "Molecular cloning of a novel G protein-coupled receptor that may  
 belong to the neuropeptide receptor family.";  
 RL FEBS Lett. 271:81-84(1990).  
 RN [2]  
 RP REVISIONS, AND FUNCTION.  
 RC TISSUE=Brain;  
 RA Krause J.E., Eva C., Seeburg P.H., Sprengel R.;  
 RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: BRAIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO TACHYKININS RECEPTORS.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL: Z11504; CAAT7579.1; -.  
 DR PIR: S12863; S12863.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 38  
 FT TRANSMEM 39 61  
 FT DOMAIN 62 71  
 FT TRANSMEM 72 93  
 FT DOMAIN 94 113  
 FT TRANSMEM 114 135  
 FT DOMAIN 136 155  
 FT TRANSMEM 156 176  
 FT DOMAIN 177 209  
 FT TRANSMEM 210 231  
 FT DOMAIN 232 262  
 FT TRANSMEM 263 285  
 FT DOMAIN 286 298  
 FT TRANSMEM 299 322  
 FT DOMAIN 323 382  
 FT CARBOHYD 2  
 FT CARBOHYD 11 11  
 FT CARBOHYD 17 17  
 FT DISULFID 112 197  
 FT LIPID 337 337  
 SQ SEQUENCE 382 AA; 44116 MW; 1D6AA038065C07C3 CRC64;  
 -----  
 Query Match 34.5%; Score 633.5; DB 1; Length 382;  
 Best local similarity 38.5%; Pred. No. 1,7e-32;  
 Matches 121; Conservative 71; Mismatches 116; Indels 6; Gaps 3;

QY 91 GNLAESDILVVFCSPEFLTSVLDOMMGFKYMGCHIMEPLQCVSLVSTLLISAIIVY 150  
 DB 79 VNLSESDLLVAVMCLPFFVYTLMDHWFGEMCKLNFPVQCVSTVTSIFSLVLAVERH 138  
 QY 151 HKIKRPIINNLNANGYFLATVWTLGPAICSPLVEFHSVLVELOFTGSALISS---RYL 207  
 DB 139 QLTINPRGMRPNRNHAYIGIVIVWLAVASSLPFVIYQILND--EPFONVSLAFAKDKYV 196  
 QY 208 CVESWPSDSYRIAFITSLIVQYLPLVCLVNVSHTSVCIRLKRNNMMDKMRNKRSSR 267  
 DB 197 CFDRFPSSHRSLSTYLLVQLQYRPEPLCFITICFKIIRLKRNNMMDKTRDSKRSSE 256  
 QY 268 SRSVFYRLLILVFAVSWMPDLHFVYVTDNDMLISNRHFKLYVCICHLGMSSCLNP 327  
 DB 257 TKRINVMLLSIVAFVAVCMCLPTFTFNVEDMNHQIATCNHLLFLCHLTAMISTCVNP 316  
 QY 328 ILVGFNLNGIRADL 341  
 DB 317 IFYGFNLKNFORDL 330  
 -----  
 RESULT 13  
 ID N6R\_RABIT STANDARD: PRT; 371 AA.  
 AC P/9217;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, last sequence update)  
 DT 30-MAY-2000 (Rel. 39, last annotation update)  
 DE Neuropeptide Y receptor type 6 (NPY6-R).  
 GN NPY6R.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Japanese white; TISSUE=skeletal muscle;  
 RX MEDLINE=97066888; PubMed=8910290;  
 RA Matsunoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiho H.,  
 RA Togami J., Kimura Y., Okada M., Yamaguchi T.;  
 RT "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in  
 RT primate species.";  
 RL J. Biol. Chem. 271:27217-27220(1996).  
 CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE  
 CC CYCLASE ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO TACHYKININS RECEPTORS.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL: D66521; BAA13104.1; -.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 34  
 FT TRANSMEM 35 57  
 FT DOMAIN 58 69  
 FT TRANSMEM 70 90  
 FT DOMAIN 91 110  
 FT TRANSMEM 111 132



QY 191 VELOETFGSALLSRVLCVESPSDYRIAFITISLLVQYILPLVCLAVSHTSVCIRLR 250  
 Db 184 -----SLEPTDIYTHQVACWEIWPSTKLNQLEFSTSLFMLOYVPLGFIILCYLKLCLRK 238  
 QY 251 RNNMMDKRDKKYSSRSRYEYRLTILILEFAVSMPLH.FHVYTDENDNISRRHKL 310  
 Db 239 RTROYDRKREKRSKLNENKRNWMLISIVTFGACWLPNTNFVLDWYHEKLSCHHDL 298  
 QY 311 VYCIHLLGMSCCLNPLLYGFLNNGIKADIVSLIH 346  
 Db 299 VFVVCILIAVSTCINPLFYGLFNKNFKQDLMLIHL 334

RESULT 15  
 NYZR.CHICK  
 ID NYZR.CHICK STANDARD: PRT: 385 AA.  
 AC Q9DDN6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).  
 GN NPY2R.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20532533; PubMed=11078884;  
 RA Salaneck E., Holmberg S.K., Berglund M.M., Boswell T., Larhammar D.;  
 RT "Chicken neuropeptide Y receptor Y2: structural and pharmacological  
 RL differences to mammalian Y2.";  
 RL FEBS Lett. 484:229-234(2000).  
 CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -!- HIGHEST TO TACHYKININS RECEPTORS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF309091; AAG37898.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECEPTOR\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 53  
 FT TRANSMEM 54 76  
 FT DOMAIN 77 86  
 FT TRANSMEM 87 108  
 FT DOMAIN 109 128  
 FT TRANSMEM 129 150  
 FT DOMAIN 151 170  
 FT TRANSMEM 171 191  
 FT DOMAIN 192 218  
 FT TRANSMEM 219 244  
 FT TRANSMEM 245 272  
 FT DOMAIN 273 295  
 FT TRANSMEM 296 308  
 FT DOMAIN 309 332  
 FT TRANSMEM 333 385  
 FT CARBOHYD 11 11  
 FT DISULFID 127 207  
 FT LIPID 346 346  
 FT PALMITATE (POTENTIAL).

SQ SEQUENCE 385 AA; 43509 MW; 60A09B314E665B62 CRC64;  
 Query Match 28.6%; Score 525; DB 1; Length 385;  
 Best Local Similarity 32.6%; Pred. No. 7,66-26;  
 Matches 99; Conservative 75; Mismatches 116; Indels 14; Gaps 4;  
 QY 49 DLQYFLGLYFVSTLGFMGNLLIMALKRNOKTTVNFILGNLAFSDIILVLECSPT 108  
 Db 52 EVQILIRAVCSIIILGIVGNSLVTHVIIFKFSMTVTNFIANLAVADLLVNTLCLEPT 111  
 QY 109 LFSVLLDQMMGKYVCHIMPLQCVSVLSTLLISTAIIVRYHMKRHSNNLANHGYF 168  
 Db 112 LVYTLGEMKLGPVLCILVPYQAALAVHSTVTLTVALDHRRCIVHLESKISRISFL 171  
 QY 169 LIATVWTGFAICSPLPVF--HSLVELOETFGSALLSRVLCVESPSD--SYRIAFIT 223  
 Db 172 IIGVAMVSAALLASPLAIFREXSLIEIIPDF-----KIYVCSKWPREGQLNGTIVSV 225  
 QY 224 SILLVQYILPLVCLTVSHTSVCIRLKRNNMMDKRDKKYSSRSRYEYRLTILILEFA 283  
 Db 226 SMLLIQYVLPALISVAYTRIMTKL--NHVSPGAGNDVHHRRQKTKMLVCVVVFA 282  
 QY 284 VSNMPLH.FHVYTDENDNISRRHKLKYCGICHLGMMSCCLNPLLYGFLNNGIKADIVS 343  
 Db 283 VSMLEPFAFQVLDSDQVLDLKEKLYTVFVFIAMCSTFANPLLYGMMNNYRTAFLT 342  
 QY 344 LIHC 347  
 Db 343 AFQC 346

Search completed: November 22, 2002, 13:09:44  
 Job time : 16 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:08:24 ; Search time 21 Seconds

(without alignments)  
1602.240 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836

Sequence: 1 MSFYSKQDYNMDELDEYYN.....GFLNNGIKADVLILHCLHM 350

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	35.1	384	2	neuropeptide Y/pep
2	637	34.7	366	2	neuropeptide Y/pep
3	633.5	34.5	349	2	G protein-coupled
4	633.5	34.5	382	2	neuropeptide Y rec
5	633.5	34.5	382	2	neuropeptide Y/pep
6	515.5	28.1	375	2	neuropeptide Y rec
7	515	28.1	375	2	neuropeptide Y/pep
8	514	28.0	375	2	pancreatic polypep
9	504	27.5	381	2	neuropeptide Y/pep
10	453.5	24.7	370	1	G protein-coupled
11	421.5	23.0	449	2	neuropeptide Y rec
12	397.5	21.7	455	2	hypothetical prote
13	365.5	19.9	423	2	glucocorticoid-ind
14	362	19.7	412	2	hypothetical prote
15	358.5	19.5	436	2	cholecystokinin-A
16	357	19.4	365	2	hypothetical prote
17	356.5	19.4	427	2	gastric CCK-A rece
18	354	19.3	444	2	hypothetical prote
19	345.5	18.8	399	2	hypothetical prote
20	345.5	18.8	443	2	glucocorticoid-ind
21	344.5	18.8	349	2	galanin receptor 1
22	344	18.7	423	2	allatostatin recep
23	341	18.6	357	2	probable allatosta
24	341	18.6	430	2	cholecystokinin A
25	340.5	18.5	391	2	hypothetical prote
26	340	18.5	398	1	neurokinin 2 recep
27	336.5	18.3	428	2	cholecystokinin ty
28	335	18.2	394	2	galanin receptor -
29	334.5	18.2	584	2	sulfakinin recepto

30	332	18.1	457	2	T29741	hypothetical prote
31	327.5	17.8	384	1	S00516	neurokinin 2 recep
32	324	17.6	402	2	I56595	neurokinin 2 recep
33	323	17.6	374	2	T19340	hypothetical prote
34	322	17.5	452	2	A46195	cholecystokinin B
35	321.5	17.5	491	2	C40470	glucocorticoid-ind
36	321	17.5	390	2	B88684	protein ACT.1 (imp
37	320	17.4	416	2	T30946	hypothetical prote
38	317	17.3	384	2	I57957	neurokinin 2 recep
39	316.5	17.2	539	2	T27559	hypothetical prote
40	312.5	17.0	384	2	S20303	neurokinin 2 recep
41	312.5	17.0	519	2	S17783	tachykinin recepto
42	312	17.0	384	2	A41007	gastrin-releasing
43	311.5	16.9	407	2	S20304	neurokinin 1 recep
44	311	16.9	453	2	S32817	gastrin receptor -
45	310.5	16.9	376	2	T19186	hypothetical prote

## ALIGNMENTS

## RESULT 1

A45490

neuropeptide Y/peptide YY receptor Y1 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Apr-2000

C:Accession: A45490; A46133; A42773

R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.

J. Biol. Chem. 268, 6703-6707, 1993

A:Title: Genomic organization, localization, and allelic differences in the gene for

A:Reference number: A45490; MUID:93203272; PMID:8095935

A:Accession: A45490

A:Molecule type: DNA

A:Residues: 1-384 <HER>

A:Note: sequence extracted from NCBI backbone (NCBI:128005, NCBI:128005)

R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992

A:Title: Cloned human neuropeptide Y receptor couples to two different second messeng

A:Reference number: A46133; MUID:92335184; PMID:1321422

A:Accession: A46133

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-384 <HEZ>

A:Note: sequence extracted from NCBI backbone (NCBI:108538)

R:Lanhammar, D.; Blomqvist, A.G.; Yee, F.; Jacin, E.; Yoo, H.; Wahlstedt, C.

J. Biol. Chem. 267, 10935-10938, 1992

A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY recep

A:Accession: A42773

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-384 <LAR>

A:Cross-references: GB:M88461; NID:9189155; PIDN:AAA73215.1; PID:9189156

A:Experimental source: fetal brain

A:Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBI:104736)

C:Genetics:

A:Gene: GDB:NPYR; NPYR

A:Cross-references: GDB:132643; OMIM:162641

A:Map position: 4q31.3-4q32

C:Superfamily: neurokinin 1 receptor

C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolest

F:37-66/Domain: transmembrane #status predicted <TM1>

F:77-103/Domain: transmembrane #status predicted <TM2>

F:118-136/Domain: transmembrane #status predicted <TM3>

F:155-179/Domain: transmembrane #status predicted <TM4>

F:209-232/Domain: transmembrane #status predicted <TM5>

F:261-286/Domain: transmembrane #status predicted <TM6>

F:300-323/Domain: transmembrane #status predicted <TM7>

F:113-198/Disulfide bonds: #status predicted

F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:338/Binding site: palmitate (Cys) (covalent) #status predicted

D	b	180	KNISDSYIGKVCLEDPEDKEFRLSYTTLTLOLGYLPCLCIFCYCRKIPLARKRRNM	239
O	y	255	MOKMRNKRSSRSRVFRLITLLIVAVSMPLHLPHVTVDFNDNLISNRHFKLYCI	314
D	b	240	MIKIRNKYSSETRKINIMLLSIYVGAFCLWPFIFILVDMMHEAVATCNHNLFELI	299
O	y	315	CHLGMSCCLNPILYGFLNNGIKADL	341
D	b	300	CHLTAMISTCVNPIFYGFLLKNKFORDL	326
 RESULT 3				
G		S12863	g protein-coupled receptor FC5 - rat	
C		C.Species:	Rattus norvegicus (Norway rat)	
C		C.Date:	12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 20-Apr-2000	
A		A.Accession:	S12863; S19101	
R		R.Eva,	C.; Keilnaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.	
F		F.FEBS Lett.	271, 81-84, 1990	
A		A.Title:	Molecular cloning of a novel G protein-coupled receptor that may belong to t	
A		A.Reference number:	S12863; MUID:91032093; PMID:2172008	
A		A.Accession:	S12863	
A		A.Molecule type:	mRNA	
A		A.Residues:	1-349 <EVA>	
A		A.Cross-references:	EMBL:Z11504	
R		R.Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.		
S		submitted to the EMBL Data Library, November 1991		
A		A.Description:	Pharmacological and transduction properties of a Recombinantly Express	
A		A.Reference number:	S19101	
A		A.Accession:	S19101	
A		A.Molecule type:	mRNA	
A		A.Residues:	1-343, 'DDDYETIAMSTMHTDYSKTSLKQASPVAKFKIMDNNEK' <KRA>	
A		A.Cross-references:	EMBL:Z11504; NID:957636; PIDN:CAAT7579.1; PID:957637	
C		C.Superfamily:	neurokinin 1 receptor	
C		C.Keywords:	G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p	
F		F.73-61/Domain:	transmembrane #status predicted <TM1>	
F		F.73-93/Domain:	transmembrane #status predicted <TM2>	
F		F.114-135/Domain:	transmembrane #status predicted <TM3>	
F		F.155-175/Domain:	transmembrane #status predicted <TM4>	
F		F.213-221/Domain:	transmembrane #status predicted <TM5>	
F		F.267-285/Domain:	transmembrane #status predicted <TM6>	
F		F.299-322/Domain:	transmembrane #status predicted <TM7>	
F		F.2,11,17/Binding site:	carbohydrate (Asn) (covalent) #status predicted	
F		F.346/Binding site:	phosphate (Thr) (covalent) #status predicted	
 Query Match                      34.5%    Score 633.5; DB 2; Length 349; Best Local Similarity         37.8%; Pred. No. 4.le-44; Matches 127; Conservative     72; Mismatches 116; Indels    21; Gaps     6;				
O	y	20	NKTL--ATENNTA---ATRNSDPFWMDYKSSVDDLOYFLGLTYF-----VSLEGFMG	68
D	b	2	NSTLESREVENSVHYNVSENSPLAFEN---DBCHLPLAVIFTTALAYGAVALILGVSG	56
O	y	69	NLLIIALLMKRNRKQTIVNPLIGMIAFSDIIVLCFSPFTTSVLIDQMFGVMCHIMP	128
D	b	57	NLAIIIIIIKKCKEMRNNTNIIIVNLSDLIIVAMCIPFFIVYITLMHMHWYFGETMCKLN	116
O	y	129	FLQCVSVALVSTLLIIISAIVRYHKIPHSINNLTANHGYFLIATVTWTGLFAICSPLPVFH	188
D	b	117	FVQCQSIVTSIFSILVLAVERHQILIINDRCWRPNRHAYIGIVYIWLAVASSLPFIYQ	176
O	y	189	SLVELOTFEGSALLS---RLCYESMPDSYIRAFITISLLVOYLIPLVCLIVSHITSYC	245
D	b	177	ILTD--EPFOVNSLAARCKKYVCFDKPRSDSHRLSYTTLLVLQYEGPLOCIFICYFKIY	234
O	y	246	IRLRNNRMMDKMNDKNYRSRSRSVYRFLTIIVLAIVASMPLHLPHVTVDFNDNLISN	305
D	b	235	IRLKRRNNMDKITDSKYRSSETKRIIVMLLSIVAFACVMDPLTIFNTYFDNNHQIIAT	294
O	y	306	RHFELVYICHLGLGMSCCLNPILYGFLNNGIKADL	341
D	b	295	CNHNLFLTCLHPTAMISTCVNPIFYGFLLKNKFORDL	326

RESULT 4  
S27388  
neuropeptide Y receptor NPY-1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Apr-2000  
C:Accession: S27388  
R:Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.  
FEBS Lett. 314, 285-288, 1992  
A:Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific exons.  
A:Reference number: S27388; MUID:93106169; PMID:1466559  
A:Accession: S27388  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-382 <EVA>  
A:Cross-references: EMBL:Z18280; NID:953438; PIDN:CAA79157.1; PID:953439  
C:Superfamily: neurokinin 1 receptor

Query Match	34.58	Score 633.5	DB 2	Length 382
Best Local Similarity	37.88	Pred. No. 4.5e-44		
Matches 127; Conservative	73	Mismatches 115;	Indels 21;	Gaps 6;

QY 20 NKIL-AEENNTA---ATRNSDFVWDYKSSVDDLOFLYFLGLYTE-----VSLGEMG 68

Db 2 NSTLFSKVENHSHYNNASENSPLAFEN-----DDCHPLAVLFTLALAYGAVIILGSG 56

QY 69 NLLIMALKKRNOKTTVNFELIGNIAFSIDILVVLECSPELTSLDLDOMEGRYACHIMP 128  
| : : : : : | : : : : : | : : : : : | : : : : : |  
Db 57 NLALIIILIKOKERNRNTNILLIVLSFSDLLVAWMLPTEFEVTYIMDHVGFENCKLNP 116

Qy 129 FLOCVSVLSTLLLSIAIVRYHMKHPISNNLTANHGFLAIATVWTGFAICSPLPVEH 188  
+ : : : : + : : : : + : : : : + : : : :  
Db 117 FVOCVSIFVSFSLIAVERHOLLINPGWRPNRRHAYIGITFIWVLVAASSIPVEITO 176

Ox 189 SLVELQETFGSALLS---RYLCVESWSPSDSYRAFTISLLVQYILPVLCTIVSHTSYC 245  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 177 ILND--EPPONNLAAPKDYCKRVCEDPKFSPDSHRSTYTLTLLLOVEGPICFIFCYCRY 234  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Dy 246 IRLKRRNNMMDKMNDKYRSRSLVPEYLLTILILEFAVSMPMLHLFHVTDENDNLISN 305  
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Dz 235 IRLKRRNNMMDKIIDSKYSRSSFEPRNTIMLSIVAFACWCLPLTFTEFNVEDNMHQTAT 294

Oy 306 RHEFLVYCICHLGLMMSCCLNPILYGFNLNGIKADL 341  
 : : : : :  
 Db 295 CNNHLLFELICHITAMISTCVNPPFYGFLINKNEPDL 330

## RESULT 5

### PARA 33

C: neuropeptide y/peptide yy receptor y1 - mouse  
C: Species: Mus musculus (house mouse)  
C: Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Apr-2000  
C: accession: B6133

A1: Title: Cloned human neuropeptide Y receptor couples to two different second messengers  
R: Herzog, H. Hort, V.J.: Ball, H.J.: Hayes, G.: Shine, J.: Settle, L.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992  
A1: Title: Cloned human neuropeptide Y receptor couples to two different second messengers  
R: Herzog, H. Hort, V.J.: Ball, H.J.: Hayes, G.: Shine, J.: Settle, L.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992

A:Accession: B46133  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Positives: 1363; 100%

A:Note: sequence extracted from NCBI backbone (NCBIP:108539)  
C:Superfamily: neurokinin 1 receptor  
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match	34.5%	Score 633.5	DB 2	Length 382
Best Local Similarity	38.5%	Pred. NO. 4.5e-44		
Matches 121; Conservative	71	Mismatches 116	Indels 6	Gaps 3

QY 32 TRNSDFPVPDDYKSSVDDQYFLIGL-YTFVSLGFMGSLLLIMALMKRNQRTVNFLLI 90  
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
19 SENSPLAFENDCHLPLAVIFLTLAAGAVIITLGVSGMALIIIIILOKEMRVNTILTI 78

Qy	91	GAASDILVYFCSPFLTSLVLLDDMMGEKVMHNPLOCVSLVSTLLSLIAVR	150
		79	VULSDDLVAAWCMPLPFVYTLDDHWVGGTKRLNPFVOCVSLVSLVLAVERH
Db			
Qy	151	HMHKPISNNLTANHGEYLATVWTGLFPAICSPLVFHSVLELOETGSAI	207
		139	QLIIPRCGRPNRHHAYIGIVYIWLVAWASSLPVYIQLTDD--EPQVNSLA
Db			
Qy	208	CYESPDSQSYRAFTISLLVOYLPLPLACLVHSFTSCIRLKRNNMMQMKR	267
		197	CPDKPSSQSHRSLYTLTLVQYGPCLCFITCYCFYIRLKRNNMMQMKR
Db			
Qy	268	SRSSVYRLTILLVFAVSMPLLFHVVTDENDMLISNRHKCYLCJHILGM	327
		257	TKRIWMLLSIVAAVACMLPLTFIENFVEDWNNQDILATCNHLLFLCHL
Db			
Qy	328	ILXGLNNGICAKDL	341
		317	IFEGFLNKNFQDRL
Db			

RESULT 6  
S63685

C:\Species: Mus musculus (house mouse)  
C:\Date: 20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Apr-2000  
C:\Accession: S63685

A:Reference number: S63685; MUID:96193913; PMID:8641440

A;Accession: 580063  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-375 <GRE>

Query Match 28.1% Score 515.5 DB 2: Length 375:  
Accession: EMBL:U0109; NID:G12Z3309; P1DN:AA02442.1; P1D:G12Z33  
C;Superfamily: neurokinin 1 receptor

OV 49 DLOYFLIGLYTEVSLIGFMGNLLIMALMKRKRNKQTTVNFELIGNAIFSDIIVLFCSPFT 108  
Best Localismilarity 32.9%; Pred. NO. 1.1/e-34;  
Matches 103; Conservative 68; Mismatches 119; Indels 23; Gaps

```

Db      39  ELAFLITTSYETILGVLGNLCLEFVTRQKEKSNVTNLLIANLAFSDFLMCLICQPLT  98
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
0v    109  L'TSVLLDOWMEKGVMCHIMPLFIOCVSVLSTLLISAIATVRYHMTKHPISNNITANHGYE  168

```

```

Db      99  VTYYIMDYWIGCEVLCKMLTFIQCMSSVNVSIILSLVLALEHRHQLIINPTGKKPSIFQAYL 158
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Ox     169  LIAVWETIGPATCSPI-----DVFH-----SLVLEIETFEFGSALLSSRYLVESWDSDSY 217

```

```

      | : | : | : | : | : | : | :
Db 159 GIVIMFISCFSLPFLANSTLNDLFHNHKSVE-----FLEDKVVCVFSWSDH 210
      | : | : | : | : | : | : | :
0v 218 PIAFTSITVOYTIPIVCIIVSHTSVCTRIKPBNNMKMDKPNKRVSSPESBVEFYBTI 277

```

```

211 RLIVTFELLLEQYCIPLAFILVCYIRIVQRLQROKHVFHAFHACSS-RAGQMKRINSMMLMT 269
378 LTVFAVSWMDHIETVYVDEENDNI TSNDEUKTIVCTGCI I GMSGCCI NPTI YGFI NGCT 337

```

```

Db 270 MVTAFAVLMPELHVFNTLEDWQGEAIPACHGNLIFLMCHDLAMASTCVNPFIIYGFNLINF 329
Ou 338 KADIVSITL---EC 347

```

Db 330 KKDIALVLTCHC 342

RESULT 7  
139182  
neuropeptide Y/peptide YY receptor Y4 - human  
G-Protein: none  
actions (max)

C; Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Apr-2000

da

5.







```

OY 143 ISIAIVRYHMIKHPISNNL--TANHGFLATVWTLGFAICSPLPVHSLVELQETGSA 200
    :|:| | | : : | :| | | :|:|:|
Db 133 VAISLERGALCRPLQSRVQTKSHALKYIAATWCLSETIMTPYIXNLPFTKNNQI 192
OY 201 LLSRYLCVESMPEDSVRIAFETISLLVOYTLPLVCLTVSHTSVCIRL-----KRRN 252
    |:| | | : : | | :|:|:| | :|:|:|
Db 193 ANMGRFL-----PSDAMQOSQOTFLLLILFLIPGVWVVAIGLISLELYOGIKFDASOKK 248
OY 253 NMMDKM-----RDNKYRSSR 267
    :|:| | | :|:|:|
Db 249 SAKKRLSSGGGGSSSSRVEDSGCYLQKSNRPKRLELQJLSTSSSGRINRIRSSG 308
OY 268 S-----RSYFRLTILILVEAVSMPLLEHVVTDPNDNLISNRHK---LVYCICHL 317
    | | | :|:|:| | | :|:|:| | :|:|:|
Db 309 SAANLIARKRYIRMLIYIVLFFLCWMPIFSANAMRAY-DTVAEKHLGTPISFIL--L 365
OY 318 LGMSCCLNPLVGLNNGIKADLYSLIHC 347
    | | | | | :|:|:|
Db 366 LSTSSCVNPLIYCFMKNRFRRLGFMATPPC 395

```

Search completed: November 22, 2002, 13:10:52  
 Job time : 23 secs

**This Page Blank (uspto)**



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:09:29 ; Search time 10 Seconds

(without alignments)  
548.152 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836  
1 MSFYSKODYNMDLEDEYNN.....GELNNGIKADVLHCLHM 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1836	100.0	350	10	US-09-771-956-6
2	1777	96.8	394	10	US-09-771-956-10
3	1743	94.9	341	10	US-09-771-956-20
4	1699	92.5	341	10	US-09-771-956-26
5	1693	92.2	383	10	US-09-771-956-21
6	1691	92.1	352	10	US-09-771-956-23
7	1668.5	90.9	455	10	US-09-771-956-13
8	1668.5	90.9	455	10	US-09-962-646-4
9	1665.5	90.7	455	10	US-09-771-956-30
10	1637	89.2	383	10	US-09-771-956-27
11	1637	89.2	395	10	US-09-771-956-25
12	1609.5	87.7	499	10	US-09-771-956-9
13	1536	83.7	456	10	US-09-962-646-2
14	1482	80.7	499	10	US-09-771-956-24
15	1461.5	79.6	508	10	US-09-771-956-22
16	1025.5	55.9	334	10	US-09-962-646-6
17	644	35.1	384	10	US-09-771-956-2
18	638	34.7	384	10	US-09-962-646-15
19	633.5	34.5	382	10	US-09-771-956-3

20	515	28.1	375	10	US-09-962-646-17	Sequence 17, Appl
21	504	27.5	381	10	US-09-962-646-16	Sequence 16, Appl
22	504	27.5	381	10	US-09-292-973-5	Sequence 5, Appl
23	504	27.5	381	10	US-09-292-973-20	Sequence 20, Appl
24	479	26.1	227	12	US-10-044-592-69	Sequence 69, Appl
25	464	25.3	370	12	US-10-044-592-12	Sequence 12, Appl
26	464	25.3	370	12	US-10-044-592-74	Sequence 74, Appl
27	429	23.4	518	10	US-09-804-551B-8	Sequence 8, Appl
28	415.5	22.6	522	10	US-09-804-551B-38	Sequence 38, Appl
29	378.5	20.6	423	8	US-08-796-570A-1	Sequence 1, Appl
30	378.5	20.6	423	9	US-10-067-477-1	Sequence 1, Appl
31	375	20.4	540	10	US-09-804-551B-2	Sequence 2, Appl
32	367	20.0	428	10	US-09-292-973-4	Sequence 4, Appl
33	366.5	20.0	426	10	US-09-292-973-19	Sequence 19, Appl
34	366.5	20.0	432	10	US-09-292-973-2	Sequence 2, Appl
35	357.5	19.5	431	10	US-09-826-508-22	Sequence 22, Appl
36	357.5	19.5	431	10	US-09-899-532-2	Sequence 2, Appl
37	333	18.1	427	10	US-09-730-931-2	Sequence 2, Appl
38	328	17.9	223	12	US-10-044-592-72	Sequence 72, Appl
39	326	17.8	223	12	US-10-044-592-71	Sequence 71, Appl
40	321	17.5	402	12	US-10-077-874-2	Sequence 19, Appl
41	321	17.5	425	10	US-09-828-538-19	Sequence 24, Appl
42	321	17.5	425	10	US-09-828-538-24	Sequence 2, Appl
43	321	17.5	425	10	US-09-961-848-2	Sequence 6, Appl
44	318	17.3	372	12	US-10-077-874-6	Sequence 2, Appl
45	317.5	17.3	389	10	US-09-828-538-20	Sequence 20, Appl

#### ALIGNMENTS

RESULT 1  
US-09-771-956-6  
; Sequence 6, Application US/09771956  
; Patent No. US20010031474A1  
GENERAL INFORMATION:  
APPLICANT: Benmett, Michele  
APPLICANT: Brodebeck, Robbin  
APPLICANT: Krause, James  
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
FILE REFERENCE: N2000 001  
CURRENT APPLICATION NUMBER: US/09/771,956  
CURRENT FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA  
US-09-771-956-6

Query Match	100.0%	Score 1836;	DB 10;	Length 350;
Best Local Similarity	100.0%	Pred. No. 8.1e-149;		
Matches 350;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSFYSKODYNMDLEDEYNNKTATENNTRSDPPVDDYKSSVDDQYFLIGLYTF	60	
DB	1	MSFYSKODYNMDLEDEYNNKTATENNTRSDPPVDDYKSSVDDQYFLIGLYTF	60	
QY	61	VSLIGFGNLLIIMALKRKRKQKTVNFIIGNLAFSIDLVLVFCSPPTLVSLDDQMF	120	
DB	61	VSLIGFGNLLIIMALKRKRKQKTVNFIIGNLAFSIDLVLVFCSPPTLVSLDDQMF	120	
QY	121	KWCHIMPFQOCVSVLSTILISIALVRYHMKRPSNNLTANHGFLATWTGLFAI	180	
DB	121	KWCHIMPFQOCVSVLSTILISIALVRYHMKRPSNNLTANHGFLATWTGLFAI	180	
QY	181	CSPLPVSFLVLEOEFPGSALLSRVLCVSWPDSRIRIAFTISLLVQYILPLVCLTFS	240	
DB	181	CSPLPVSFLVLEOEFPGSALLSRVLCVSWPDSRIRIAFTISLLVQYILPLVCLTFS	240	

Qy	24.1	HTSWCIRLKRNNNMDDKROKKYSSSSRSFYETLLITLVEFAWMDLPHFYVDND	300
Db	24.1	HTSWCIRLKRNNNMDDKROKKYSSSSRSFYETLLITLVEFAWMDLPHFYVDND <td>3000</td>	3000
Qy	30.1	NLISNRHKKLYVCIICHLGMMSSCLNPLVGLFNGIKADVLSITICLHM	350
Db	30.1	NLISNRHKKLYVCIICHLGMMSSCLNPLVGLFNGIKADVLSITICLHM	350

RESULT 2  
 US-09-771-956-10  
 : Sequence 10, Application US/09771956  
 : Patent No. US20010031474A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Bennett, Michele  
 : APPLICANT: Brodbeck, Robbin  
 : APPLICANT: Krause, James  
 : TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 : FILE REFERENCE: N2000.001  
 : CURRENT APPLICATION NUMBER: US/09/771,956  
 : CURRENT FILING DATE: 2001-01-29  
 : NUMBER OF SEQ ID NOS: 31  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 10  
 : LENGTH: 394  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA  
 : US-09-771-956-10

Query Match	96.8%:	Score 1777:	DB 10:	Length 394:
Best Local Similarity	99.4%:	Pred. No. 9.4e-144:		
Matches 339:	Conservative 1:	Mismatches 1:	Indels 0:	Gaps 0:
QY	1	MSFYSKODYNMNDELDEDEYNNKTATENNNTAAARNSDPFVWDQKSSVDDLOQYFLIGLYTE	60	
Db	1	MSFYSKQOYNNMDELDEDEYNNKTATENNNTAAARNSDPFVWDQKSSVDDLOQYFLIGLYTE	60	
QY	61	VSLIGFPGNLLILMAIMKKRNQKTTVNFILIGNLAFSDIILVLECSGFITTSVLLDQMMFG	120	
Db	61	VSLIGFPGNLLILMAIMKKRNQKTTVNFILIGNLAFSDIILVLECSGFITTSVLLDQMMFG	120	
QY	121	KVMCHIMPELDCSVLSTVTLILSTAIYRHYHIKHPISNNITANGGYFLIAVMTLGAFL	180	
Db	121	KVMCHIMPELDCSVLSTVTLILSTAIYRHYHIKHPISNNITANGGYFLIAVMTLGAFL	180	
QY	181	CSPLPVFHSIVLEQETTESFSAIISRYLCEVESPSDSYRIFAFTISLLVYLILPECLVYS	240	
Db	181	CSPLPVFHSIVLEQETTESFSAIISRYLCEVESPSDSYRIFAFTISLLVYLILPECLVYS	240	
QY	241	HTSVICIRLKRNNMMKDKRDNKYRSSRSRSYVRLTILILVFAVSMPLHLEFHVVDEND	300	
Db	241	HTSVICIRLKRNNMMKDKRDNKYRSSRSRSYVRLTILILVFAVSMPLHLEFHVVDEND	300	
QY	301	NLISNRHFKILVYCTCHLLGMSSCLNPLLYGFLNNGICADL 341		
Db	301	NLISNRHFKILVYCTCHLLGMSSCLNPLLYGFLNNGICADL 341		

```

RESULT 3
US-09-771-956-20
; Sequence 20, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000 001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31

```

```

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-20

```

Query Match	94.9%	Score 1743	DB 10	Length 341
Best Local Similarity	97.6%	Pred. No. 6.1e-141		
Matches 332	4	Mismatches	4	Indels 0
				Gaps 0

Qy	11	MDLEDEYNTLATENTTAATRNDSDFPMDQYSSVDDQYFLIGLXTYFVSLGFGNL	70
Dd	1	MDLELDYNTLATENTTAATRNDSDFPMDQYSSVDDQYFLIGLXTYFVSLGFGNL	60
Qy	71	LILALMRKNOKTTVNF.LIGNLAFSDILV.LFCSPEFTLSVLLDDQMFCKMCHMPL	130
Dd	61	LILALMRKNOKTTVNF.LIGNLAFSDILV.LFCSPEFTLSVLLDDQMFCKMCHMPL	120
Qy	131	OCVSALVSTLLISLAIAYRYMHKIPISNNLTANHGFELATVWTGLFALCISPLPVFHS	190
Dd	121	OCVSALVSTLLISLAIAYRYMHKIPISNNLTANHGFELATVWTGLFALCISPLPVFHS	180
Qy	191	VELOETFGSALLSSRYLCVESWPSDSYRIAFETISLLVQYTLPLVCLTVSHTSYCIRLKR	250
Dd	181	VELOETFGSALLSSRYLCVESWPSDSYRIAFETISLLVQYTLPLVCLTVSHTSYCIRLKR	240
Qy	251	RNNMMDKKRDKYRSSRSRYFRTLLILVFAVSMPDILFHVYTPDNBLISNRHFKL	310
Dd	241	RNNMMDKKRDKYRSSRSRYFRTLLILVFAVSMPDILFHVYTPDNBLISNRHFKL	300
Qy	311	YVCICHLGMMSCCLNPLTGVFLNNGIKADLVSLIHCILHM	350
Dd	301	YVCICHLGMMSCCLNPLTGVFLNNGIKADLVSLIHCILHM	340

RESULT 4  
 US-09-771-956-26  
 Sequence 26, Application US/09771956  
 Patent No. US20010031474A1  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, Michele  
 APPLICANT: Brodbeck, Robbin  
 APPLICANT: Krause, James  
 TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 FILE REFERENCE: N2000.001  
 CURRENT APPLICATION NUMBER: US/09/771,956  
 CURRENT FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 26  
 LENGTH: 341  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERAN  
 US-09-771-956-26

[illegible]

```

Db 121 QCVTVLSTLILSLIAIVRYHMKHPVSNMLTANHGFLATVWTGLATCSPLPVFHSI 180
QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 240
QY 251 RNNMMDKMRDNKRRSSRSRSVFRITLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 310
Db 241 RNNMMDKMRDNKRRSSRSRSVFRITLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 300
QY 311 VVCICHLGMMSCCLNPILYGFNLNGIKADLSLHCLHM 350
Db 301 VVCICHLGMMSCCLNPILYGFNLNGIKADLSLHCLHM 340

RESULT 5
US-09-771-956-21
; Sequence 21, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-21

Query Match          92.2%; Score 1693; DB 10; Length 383;
Best Local Similarity 97.6%; Pred. No. 1.2e-136;
Matches 333; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 MDLEDEYTKTLATENNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTVFVSLGEGNL 70
Db 1 MDLEQDFYKKTLATENNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTVFVSLGEGNL 60
QY 71 LILMALMKRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMFGKVMCHIMPEL 130
Db 61 LILMALMKRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMFGKVMCHIMPEL 120
QY 131 QCVSVLSTLILSLIAIVRYHMKHPISNNMLTANHGFLATVWTGLATCSPLPVFHSI 190
Db 121 QCVSVLSTLILSLIAIVRYHMKHPISNNMLTANHGFLATVWTGLATCSPLPVFHSI 180
QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 240
QY 251 RNNMMDKMRDNKRRSSRSRSVFRITLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 310
Db 241 RNNMMDKMRDNKRRSSRSRSVFRITLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 300
QY 311 VVCICHLGMMSCCLNPILYGFNLNGIKADL 341
Db 301 VVCICHLGMMSCCLNPILYGFNLNGIKADL 331

RESULT 6
US-09-771-956-23
; Sequence 23, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
```

```

; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-23

Query Match          92.1%; Score 1691; DB 10; Length 352;
Best Local Similarity 92.4%; Pred. No. 1.6e-136;
Matches 318; Conservative 16; Mismatches 10; Indels 0; Gaps 0;
```

```

QY 7 QDYNMDELDYNYKTLATENNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTVFVSLGEG 66
Db 8 QDSMEFKLEHFNKTEVTENNNTAARNAPAMEDYRGVDDIQYFLIGLYTVFVSLGEG 67
QY 67 MGNLILMALMKRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMFGKVMCHI 126
Db 68 MGNLILMALMKRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMFGKVMCHI 127
QY 127 MPFLQCVSVLSTLILSLIAIVRYHMKHPISNNMLTANHGFLATVWTGLATCSPLPV 186
Db 128 MPFLQCVSVLSTLILSLIAIVRYHMKHPISNNMLTANHGFLATVWTGLATCSPLPV 187
QY 187 FHSI VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVC 246
Db 188 FHSI VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVC 247
QY 247 RLRKRRNMMDKMRDNKRRSSRSRSVFRITLILVFAVSWMPHLFHVYTDNDNLISNR 306
Db 248 RLRKRRNMMDKMRDNKRRSSRSRSVFRITLILVFAVSWMPHLFHVYTDNDNLISNR 307
QY 307 HFKLVYICICHLGMMSCCLNPILYGFNLNGIKADLSLHCLHM 350
Db 308 HFKLVYICICHLGMMSCCLNPILYGFNLNGIKADLSLHCLHM 351
```

```

RESULT 7
US-09-771-956-13
; Sequence 13, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-956-13

Query Match          90.9%; Score 1668.5; DB 10; Length 455;
Best Local Similarity 73.2%; Pred. No. 1.8e-134;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
```

```

QY 1 MSFYSKODYNMDELDYNYKTLATENNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTF 60
Db 1 MSFYSKODYNMDELDYNYKTLATENNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTF 60
```



QY 316 HLGMSCLNPILYGFLNNGIKADIYLIHCLHM 350  
 Db 421 HLGMSCLNPILYGFLNNGIKADIMSLHCLHM 455

RESULT 10

US-09-771-956-27  
 ; Sequence 27, Application US/09771956  
 ; Patent No. US20010031474A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, Michele  
 ; APPLICANT: Brobeck, Robbin  
 ; APPLICANT: Krause, James  
 ; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 ; FILE REFERENCE: N2000.001  
 ; CURRENT APPLICATION NUMBER: US/09/771.956  
 ; CURRENT FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: Patentln Ver. 2.1  
 ; SEQ ID NO 27  
 ; LENGTH: 383  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA  
 US-09-771-956-27

Query Match 89.7%; Score 1647; DB 10; Length 383;  
 Best Local Similarity 94.0%; Pred. No. 9, 8e-133;  
 Matches 311; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 11 MDLEDEYKNTLATENNATATRNNDSPVVDYKSSVDLQYFLIGLYTFVSLGFMGNL 70  
 Db 1 MGSEIDPYKKTTLASENNVTATRNNGEPVWEDYKGSVDLQYFLIGLYTFVSLGFMGNL 60  
 QY 71 LILMALKKRNKQKTVNPLGNLAFSIDLVLVLCSPPTLTVSLLDQMFEGVMCHIMPL 130  
 Db 61 LILMAVRRKRNKQKTVNPLGNLAFSIDLVLVLCSPPTLTVSLLDQMFEGVMCHIMPL 120  
 QY 131 QCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATVWTGLGFAICSPLPVHSL 190  
 Db 121 QCVTVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATVWTGLGFAICSPLPVHSL 180  
 QY 191 VELOETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVICRLKR 250  
 Db 181 VELOESFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVICRLKR 240  
 QY 251 RNNMMDKRNKRYRSRSRVFRLTLLLVFANVMPLHFLHVYVDFNDNLISNRHFKL 310  
 Db 241 RNNMMDKRNKRYRSRSRVFRLTLLLVFANVMPLHFLHVYVDFNDNLISNRHFKL 300  
 QY 311 VYICHLHGMSCCLNPILYGFLNNGIKADL 341  
 Db 301 VYICHLHGMSCCLNPILYGFLNNGIQRD 331

RESULT 11

US-09-771-956-25  
 ; Sequence 25, Application US/09771956  
 ; Patent No. US20010031474A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, Michele  
 ; APPLICANT: Brobeck, Robbin  
 ; APPLICANT: Krause, James  
 ; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 ; FILE REFERENCE: N2000.001  
 ; CURRENT APPLICATION NUMBER: US/09/771.956  
 ; CURRENT FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: Patentln Ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 395  
 ; TYPE: PRT

; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA  
 US-09-771-956-25

Query Match 89.2%; Score 1637; DB 10; Length 395;  
 Best Local Similarity 92.8%; Pred. No. 7, 2e-132;  
 Matches 308; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 7 QDYNMDELDEYKNTLATENNATATRNNDSPVVDYKSSVDLQYFLIGLYTFVSLGFM 66  
 Db 8 QDSSMEKLEHFNKTVTENNATAARNAAPAMEDRGSDVDLQYFLIGLYTFVSLGFM 67  
 QY 67 MGNLILMALMKRNKQKTVNPLGNLAFSIDLVLVLCSPPTLTVSLLDQMFEGVMCHI 126  
 Db 68 MGNLILMAVKKRNKQKTVNPLGNLAFSIDLVLVLCSPPTLTVSLLDQMFEGVMCHI 127  
 QY 127 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATVWTGLGFAICSPLPV 186  
 Db 128 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATVWTGLGFAICSPLPV 187  
 QY 187 FHSVLQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVICI 246  
 Db 188 FHSVLQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVICI 247  
 QY 247 RLKRRNMDKRNKRYRSRSRVFRLTLLLVFANVMPLHFLHVYVDFNDNLISNR 306  
 Db 248 RLKRRNMDKRNKRYRSRSRVFRLTLLLVFANVMPLHFLHVYVDFNDNLISNR 307  
 QY 307 HFKLVYICHLHGMSCCLNPILYGFLNNGIK 338  
 Db 308 HFKLVYICHLHGMSCCLNPILYGFLNNGIK 339

RESULT 12

US-09-771-956-9  
 ; Sequence 9, Application US/09771956  
 ; Patent No. US20010031474A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, Michele  
 ; APPLICANT: Brobeck, Robbin  
 ; APPLICANT: Krause, James  
 ; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 ; FILE REFERENCE: N2000.001  
 ; CURRENT APPLICATION NUMBER: US/09/771.956  
 ; CURRENT FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: Patentln Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 499  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA  
 US-09-771-956-9

Query Match 87.7%; Score 1609.5; DB 10; Length 499;  
 Best Local Similarity 72.2%; Pred. No. 2e-129;  
 Matches 322; Conservative 7; Mismatches 12; Indels 105; Gaps 3;

QY 1 MSFYKODYNMDELDEYKNTLATENNATATRNNDSPVVDYKSSVDLQYFLIGLYTF 60  
 Db 1 MSFYKODYNMDELDEYKNTLATENNATATRNNDSPVVDYKSSVDLQYFLIGLYTF 60  
 QY 61 VSLIGFEGNLLILMALMKRNKQKTVNPLGNLAFSIDLVLVLCSPPTLTVSLLDQMFEG 120  
 Db 61 VSLIGFEGNLLILMALMKRNKQKTVNPLGNLAFSIDLVLVLCSPPTLTVSLLDQMFEG 120  
 QY 121 KVMCHIMPLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATVWTGLGFAI 180  
 Db 121 KVMCHIMPLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATVWTGLGFAI 180  
 QY 181 CSPLPVHSLVLEQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVS 240

Db 181 CSPLPEFHSVLVELOETFGSALLSRKLCVESWPSDSYRIAFITSLLYOYLPLVCLTVS 240  
Qy 241 HTSVC-----IRLKRNNMMDK----- 257  
Db 241 HTSVCRSISCSLSKKNENLEENEMINTLPHSKSGSPOVKLSGSHKWSYFIKKHRRYS 300  
Qy 258 -----MRDNKYR----- 264  
Db 301 KKTACVLPAPERPEQENHSRIILPENFGSVRSQLSSSSKFIDCVPTCFELKPENSDVHEL 360  
Qy 265 -----SRSRSVFRLTLLILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYIC 315  
Db 361 RKRKRSVTRIKRKSRSVFRITLLILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYIC 420  
Qy 316 HLGMMSCCLNPILYGFNLNGIKADL 341  
Db 421 HLGMMSCCLNPILYGFNLNGIQRDL 446

RESULT 13  
US-09-962-646-2  
; Sequence 2, Application US/09962646  
; Patent No. US20020103123A1  
; GENERAL INFORMATION:  
; APPLICANT: GERALD, CHRISTOPHE P.G.  
; APPLICANT: WEINSHANK, RICHARD L.  
; APPLICANT: WALKER, MARY W  
; APPLICANT: BRANCHER, THERESA  
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND  
; FILE REFERENCE: 1795/46166BA  
; CURRENT APPLICATION NUMBER: US/09/962, 646  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/200, 673  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 08/566, 096  
; PRIOR FILING DATE: 1995-12-01  
; PRIOR APPLICATION NUMBER: 08/349, 025  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 456  
; TYPE: PRT  
; ORGANISM: Rattus No. US20020103123A1veglicus  
US-09-962-646-2

Query Match 83.7%; Score 1536; DB 10; Length 456;  
Best Local Similarity 67.9%; Pred. No. 3.1e-123;  
Matches 304; Conservative 21; Mismatches 19; Indels 104; Gaps 3;  
Qy 7 ODYMDLELDYUKTLATENNATRSDEPVDYKSSVDDLOYLFLIGLYTVSLIGF 66  
Db 8 QDSSMERLEHFNKTYTENNATAARNAAPAMEDYRGVDDLOYLFLIGLYTVSLIGF 67  
Qy 67 MGNLLILMALKKRNOKTYVNLIGNLAFSDILVLFCSPTLTSVLLDQMFQKVMCHI 126  
Db 68 MGNLLILMAVKKRNOKTYVNLIGNLAFSDILVLFCSPTLTSVLLDQMFQKVMCHI 127  
Qy 127 MPFLQCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 186  
Db 128 MPFLQCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 187  
Qy 187 FHSVLVELOETFGSALLSRKLCVESWPSDSYRIAFITSLLYOYLPLVCLTVSHTSVC- 245  
Db 188 FHSVLVELOETFGSALLSRKLCVESWPSDSYRIAFITSLLYOYLPLVCLTVSHTSVC- 247  
Qy 246 ---IRLKRNNMMDK-----MRDNKYRS----- 266  
Db 248 SISGSLSHKRNLEENEMINTLQPSKSKRNQAKTPSTQKWSYFIKRHRRRYSKKTACV 307  
Qy 267 ----- 266

Db 308 LPAPAGSQGKHLAVPENPASVRSQLSPPSKVPIGVPICFEVKEPDESSDAHEMRKRSIT 367  
Qy 267 ---SRSRSVFRLTLLILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYICICHLGMS 322  
Db 368 RIKRKSRSVFRITLLILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYICICHLGMS 427  
Qy 323 CCLNPILYGFNLNGIKADLVSLIHLHM 350  
Db 428 CCLNPILYGFNLNGIKADLVSLIHLHM 455

RESULT 14  
US-09-771-956-24  
; Sequence 24, Application US/09771956  
; Patent No. US20010031474A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michele  
; APPLICANT: Brobeck, Robbin  
; APPLICANT: Krause, James  
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
; FILE REFERENCE: N2000-001  
; CURRENT APPLICATION NUMBER: US/09/771, 956  
; CURRENT FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA  
US-09-771-956-24

Query Match 80.7%; Score 1482; DB 10; Length 499;  
Best Local Similarity 67.4%; Pred. No. 1.3e-118;  
Matches 294; Conservative 20; Mismatches 18; Indels 104; Gaps 3;  
Qy 7 ODYMDLELDYUKTLATENNATRSDEPVDYKSSVDDLOYLFLIGLYTVSLIGF 66  
Db 8 QDSSMERLEHFNKTYTENNATAARNAAPAMEDYRGVDDLOYLFLIGLYTVSLIGF 67  
Qy 67 MGNLLILMALKKRNOKTYVNLIGNLAFSDILVLFCSPTLTSVLLDQMFQKVMCHI 126  
Db 68 MGNLLILMAVKKRNOKTYVNLIGNLAFSDILVLFCSPTLTSVLLDQMFQKVMCHI 127  
Qy 127 MPFLQCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 186  
Db 128 MPFLQCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 187  
Qy 187 FHSVLVELOETFGSALLSRKLCVESWPSDSYRIAFITSLLYOYLPLVCLTVSHTSVC- 245  
Db 188 FHSVLVELOETFGSALLSRKLCVESWPSDSYRIAFITSLLYOYLPLVCLTVSHTSVC- 247  
Qy 246 ---IRLKRNNMMDK-----MRDNKYRS----- 266  
Db 248 SISGSLSHKRNLEENEMINTLQPSKSKRNQAKTPSTQKWSYFIKRHRRRYSKKTACV 307  
Qy 267 ----- 266  
Db 308 LPAPAGSQGKHLAVPENPASVRSQLSPPSKVPIGVPICFEVKEPDESSDAHEMRKRSIT 367  
Qy 267 ---SRSRSVFRLTLLILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYICICHLGMS 322  
Db 368 RIKRKSRSVFRITLLILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYICICHLGMS 427  
Qy 323 CCLNPILYGFNLNGIK 338  
Db 428 CCLNPILYGFNLNGIK 443  
RESULT 15  
US-09-771-956-22



**This Page Blank (uspto)**



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:08:44 ; Search time 14 Seconds  
(without alignments)  
735.573 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836  
Sequence: 1 MSFYSKQDYNMDELDELYNN.....GFLNNGIKADLVSLHCLHM 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1668.5	90.9	455	1	US-08-349-025-4
2	1668.5	90.9	455	2	US-08-566-096A-4
3	1668.5	90.9	455	2	US-08-668-650B-4
4	1668.5	90.9	455	4	US-09-200-673-4
5	1668.5	90.9	456	5	PCT-US95-15646-4
6	1616.5	88.0	456	2	US-08-668-650B-14
7	1613.5	87.9	445	2	US-08-630-118A-6
8	1613.5	87.9	445	2	US-08-838-399-6
9	1613.5	87.9	445	2	US-09-003-199-21
10	1613.5	87.9	445	4	US-09-235-839-6
11	1613.5	87.9	445	4	US-09-327-035-6
12	1610.5	87.7	445	4	US-09-040-958-2
13	1610.5	87.7	445	4	US-09-040-958-4
14	1549.5	84.4	445	2	US-09-003-199-2
15	1536	83.7	456	1	US-08-349-025-2
16	1536	83.7	456	2	US-08-566-096A-2
17	1536	83.7	456	2	US-08-668-650B-2
18	1536	83.7	456	4	US-09-200-673-2
19	1536	83.7	456	5	PCT-US95-15646-2
20	1526	83.1	445	2	US-08-630-118A-4
21	1526	83.1	445	2	US-08-838-399-4
22	1526	83.1	445	2	US-09-003-199-23
23	1526	83.1	445	4	US-09-235-839-4
24	1526	83.1	445	4	US-09-327-035-4
25	1519	82.7	445	2	US-08-630-118A-2
26	1519	82.7	445	2	US-08-838-399-2
27	1519	82.7	445	4	US-09-235-839-2

28	1519	82.7	445	4	US-09-327-035-2	Sequence 2, App11
29	1025.5	55.9	334	2	US-08-566-096A-6	Sequence 6, App11
30	1025.5	55.9	334	2	US-08-668-650B-6	Sequence 6, App11
31	1025.5	55.9	334	4	US-09-200-673-6	Sequence 6, App11
32	1025.5	55.9	334	5	PCT-US95-15646-6	Sequence 6, App11
33	644	35.1	383	3	US-09-045-186-2	Sequence 2, App11
34	644	35.1	384	1	US-08-232-144-4	Sequence 4, App11
35	644	35.1	384	2	US-08-555-268A-15	Sequence 15, App1
36	644	35.1	384	5	PCT-US93-05039-3	Sequence 3, App11
37	638	34.7	384	4	US-09-200-673-15	Sequence 15, App1
38	633.5	34.5	382	1	US-08-415-818-7	Sequence 7, App11
39	633.5	34.5	382	2	US-08-894-236-7	Sequence 7, App11
40	633.5	34.5	382	2	US-08-555-268A-13	Sequence 13, App1
41	633.5	34.5	382	2	US-08-555-268A-14	Sequence 14, App1
42	633.5	34.5	382	5	PCT-US96-01444-7	Sequence 7, App11
43	620	33.8	411	5	US-08-817-869-3	Sequence 3, App11
44	620	33.8	411	5	PCT-US95-14377-3	Sequence 3, App11
45	552.5	30.1	371	1	US-08-415-818-6	Sequence 6, App11

## ALIGNMENTS

```
RESULT 1
US-08-349-025-4
; Sequence 4, Application US/08349025
; Patent No. 5602024
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Walker, Mary W.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinschank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
; TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YX RECEPTOR (Y5) AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,025
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1795/46166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-025-4

Query Match: 90.9%; Score 1668.5; DB 1; Length 455;
Best local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 1 MSFYSKQDYNMDELDELYNNKTLATENRATRNDFPWWDKSSVDLQYFLIGLYTF 60
|||||
```

Db 1 MSFYSKODYNMDLEDEYYNKTLATENNATRNDSDFPVDYKSSVDDLOYLGLTYF 60  
QY 61 VSLGFMGNLLILMALMKRNOKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDDQWMEG 120  
Db 61 VSLGFMGNLLILMALMKRNOKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDDQWMEG 120  
QY 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKIPISNNLTANNGYFLIATVWTIGFAI 180  
Db 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKIPISNNLTANNGYFLIATVWTIGFAI 180  
QY 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
Db 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
QY 241 HTSVC---ITLKRNNMDK----- 257  
Db 241 HTSVCRSISGCLSNKENLEENIMINTLHPSSKSGPOVKLSGSHKWSYFIKKHRRYS 300  
QY 258 -----MRDNKYY----- 264  
Db 301 KKTACVLPAPRPSOENSRLLPENFGSVRSQSSSKFICGPTCFEIKPEENSDVHEL 360  
QY 265 -----SSRSVFEYRTILILVFAVSWMPHLFHVYTDENDNISNRHFKLVYCIC 315  
Db 361 RVKRSVTRIKKRSRSVEFRTILILVFAVSWMPHLFHVYTDENDNISNRHFKLVYCIC 420  
QY 316 HLLGMSCCLNPILYGLFNGIKADIVSLIHCLHM 350  
Db 421 HLLGMSCCLNPILYGLFNGIKADIVSLIHCLHM 455

RESULT 2  
US-08-566-096A-4  
Sequence 4, Application US/08566096A  
Patent No. 5968819  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe P.G.  
APPLICANT: Walker, Mary W.  
APPLICANT: Branchek, Theresa  
APPLICANT: Weinshank, Richard L.  
TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR,  
TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC  
TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YX RECEPTOR (Y5) AND USES THEREOF  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,096A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/46166-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-566-096A-4  
Query Match 90.9%; Score 1668.5; DB 2; Length 455;  
Best Local Similarity 73.2%; Pred. No. 8.8e-135;  
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 1 MSFYSKODYNMDLEDEYYNKTLATENNATRNDSDFPVDYKSSVDDLOYLGLTYF 60  
Db 1 MSFYSKODYNMDLEDEYYNKTLATENNATRNDSDFPVDYKSSVDDLOYLGLTYF 60  
QY 61 VSLGFMGNLLILMALMKRNOKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDDQWMEG 120  
Db 61 VSLGFMGNLLILMALMKRNOKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDDQWMEG 120  
QY 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKIPISNNLTANNGYFLIATVWTIGFAI 180  
Db 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKIPISNNLTANNGYFLIATVWTIGFAI 180  
QY 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
Db 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
QY 241 HTSVC---ITLKRNNMDK----- 257  
Db 241 HTSVCRSISGCLSNKENLEENIMINTLHPSSKSGPOVKLSGSHKWSYFIKKHRRYS 300  
QY 258 -----MRDNKYY----- 264  
Db 301 KKTACVLPAPRPSOENSRLLPENFGSVRSQSSSKFICGPTCFEIKPEENSDVHEL 360  
QY 265 -----SSRSVFEYRTILILVFAVSWMPHLFHVYTDENDNISNRHFKLVYCIC 315  
Db 361 RVKRSVTRIKKRSRSVEFRTILILVFAVSWMPHLFHVYTDENDNISNRHFKLVYCIC 420  
QY 316 HLLGMSCCLNPILYGLFNGIKADIVSLIHCLHM 350  
Db 421 HLLGMSCCLNPILYGLFNGIKADIVSLIHCLHM 455  
RESULT 3  
US-08-668-650B-4  
Sequence 4, Application US/08668650B  
Patent No. 5989920  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe P.G.  
APPLICANT: Walker, Mary W.  
APPLICANT: Branchek, Theresa  
APPLICANT: Weinshank, Richard L.  
TITLE OF INVENTION: Methods of Modifying Feeding Behavior,  
TITLE OF INVENTION: Compounds Useful in Such Methods, and DNA Encoding a  
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YX Receptor  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668,650B  
FILING DATE: 04-JUN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/46166C

```

TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 212-278-0400
: TELEFAX: 212-391-0525
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 455 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-668-6508-4

Query Match      90.9%; Score 1668.5; DB 2; Length 455;
Best Local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 1 MSFYSKODYNMDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOYLIGLYTF 60
   1 MSFYSKODYNMDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOYLIGLYTF 60
DB 1 MSFYSKODYNMDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOYLIGLYTF 60
QY 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVYFCSPTLTSLVLDQMMFG 120
   61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVYFCSPTLTSLVLDQMMFG 120
DB 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVYFCSPTLTSLVLDQMMFG 120
QY 121 KVMCHIMFLOCVSVLSTLLISAIYRYMHIKHPISNNLTANHGFLLIATVMTLGFAT 180
   121 KVMCHIMFLOCVSVLSTLLISAIYRYMHIKHPISNNLTANHGFLLIATVMTLGFAT 180
DB 121 KVMCHIMFLOCVSVLSTLLISAIYRYMHIKHPISNNLTANHGFLLIATVMTLGFAT 180
QY 181 CSPLPVFHSVLELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
   181 CSPLPVFHSVLELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVFHSVLELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVC---IRLKRNNMMDK----- 257
   241 HTSVC---IRLKRNNMMDK----- 257
DB 241 HTSVC---IRLKRNNMMDK----- 257
QY 258 -----MRDNKYR----- 264
   258 -----MRDNKYR----- 264
DB 301 KKTACVLPAPRPSQENHSRLPENFGSVRSQSSSKFIPGVTCEIKKEPENSVDHEL 360
   301 KKTACVLPAPRPSQENHSRLPENFGSVRSQSSSKFIPGVTCEIKKEPENSVDHEL 360
QY 361 RVKRSVTRIKRRSRVFRLLTLLVFAVSWMPLHLFHVYDFDNDNLISNHFLLVYCIC 420
   361 RVKRSVTRIKRRSRVFRLLTLLVFAVSWMPLHLFHVYDFDNDNLISNHFLLVYCIC 420
DB 421 HLLGMMSCLNPILYGLFNGIKADLVSLIHCLHM 455
   421 HLLGMMSCLNPILYGLFNGIKADLVSLIHCLHM 455

RESULT 4
US-09-200-673-4
: Sequence 4, Application US/09200673A
: Patent No. 6316203
: GENERAL INFORMATION:
: APPLICANT: Gerald, Christophe P.G.
: APPLICANT: Weissbank, Richard L.
: APPLICANT: Walker, Mary W.
: APPLICANT: Branchek, Theresa
: TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
: TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic
: TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide Y Receptor (Y5)
: FILE REFERENCE: 4616-B2/JPM
: CURRENT APPLICATION NUMBER: US/09/200, 673A
: CURRENT FILING DATE: 1998-11-25
: EARLIER APPLICATION NUMBER: 08/566, 096
: EARLIER FILING DATE: 1995-12-01
: EARLIER APPLICATION NUMBER: 08/349, 025
: EARLIER FILING DATE: 1994-12-02
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 455
: TYPE: PRT
: ORGANISM: Homo sapiens

```

```

US-09-200-673-4
Query Match      90.9%; Score 1668.5; DB 4; Length 455;
Best Local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 1 MSFYSKODYNMDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOYLIGLYTF 60
   1 MSFYSKODYNMDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOYLIGLYTF 60
DB 1 MSFYSKODYNMDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOYLIGLYTF 60
QY 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVYFCSPTLTSLVLDQMMFG 120
   61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVYFCSPTLTSLVLDQMMFG 120
DB 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVYFCSPTLTSLVLDQMMFG 120
QY 121 KVMCHIMFLOCVSVLSTLLISAIYRYMHIKHPISNNLTANHGFLLIATVMTLGFAT 180
   121 KVMCHIMFLOCVSVLSTLLISAIYRYMHIKHPISNNLTANHGFLLIATVMTLGFAT 180
DB 121 KVMCHIMFLOCVSVLSTLLISAIYRYMHIKHPISNNLTANHGFLLIATVMTLGFAT 180
QY 181 CSPLPVFHSVLELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
   181 CSPLPVFHSVLELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVFHSVLELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVC---IRLKRNNMMDK----- 257
   241 HTSVC---IRLKRNNMMDK----- 257
DB 241 HTSVC---IRLKRNNMMDK----- 257
QY 258 -----MRDNKYR----- 264
   258 -----MRDNKYR----- 264
DB 301 KKTACVLPAPRPSQENHSRLPENFGSVRSQSSSKFIPGVTCEIKKEPENSVDHEL 360
   301 KKTACVLPAPRPSQENHSRLPENFGSVRSQSSSKFIPGVTCEIKKEPENSVDHEL 360
QY 361 RVKRSVTRIKRRSRVFRLLTLLVFAVSWMPLHLFHVYDFDNDNLISNHFLLVYCIC 420
   361 RVKRSVTRIKRRSRVFRLLTLLVFAVSWMPLHLFHVYDFDNDNLISNHFLLVYCIC 420
DB 421 HLLGMMSCLNPILYGLFNGIKADLVSLIHCLHM 455
   421 HLLGMMSCLNPILYGLFNGIKADLVSLIHCLHM 455

RESULT 5
PCT-US95-15646-4
: Sequence 4, Application PC/TUS9515646
: GENERAL INFORMATION:
: APPLICANT: Synaptic Pharmaceutical Corporation
: TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS
: TITLE OF INVENTION: USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC ATY
: TITLE OF INVENTION: Y/PEPTIDE Y RECEPTOR (Y5) AND USES THEREOF
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCY/US95/15646
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 1795/46166-A-PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:

```

LENGTH: 456 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-15646-4

Query Match 90.9%; Score 1668.5; DB 5; Length 456;  
Best Local Similarity 73.2%; Pred. No. 8.8e-135;  
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 1 MSFYSKODYNNDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOQYFLIGLYTF 60  
DB 1 MSFYSKODYNNDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOQYFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALMKRRKQKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLDQMMFG 120  
DB 61 VSLGFMGNLLILMALMKRRKQKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLDQMMFG 120  
QY 121 KVMCHIMFLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLIATVWTGFAI 180  
DB 121 KVMCHIMFLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLIATVWTGFAI 180  
QY 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240  
DB 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240  
QY 241 HTSVC---IRLKRNNMMDK----- 257  
DB 241 HTSVCRTISGSLSNKENLEENEMINTLPFKSKGPQVKLSSHKMSYSFIKKRRRYS 300  
QY 258 -----MRDNKRY----- 264  
DB 301 KKTACVLPAPARPOENHSRLPENFGSVRSQSSSKFTIGVPTCFEIKPENSDVHEL 360  
QY 265 -----SSRSRSVEYRLTILILVFAVSWMPHLHFVVTDFDNDLISNRHFKLVYCIC 315  
DB 361 RVKRSVTRIKRKSRSVYRLTILILVFAVSWMPHLHFVVTDFDNDLISNRHFKLVYCIC 420  
QY 316 HLLGMSCCLNPILYGFNLNGIKADLVSLIQLCHM 350  
DB 421 HLLGMSCCLNPILYGFNLNGIKADLVSLIQLCHM 455

RESULT 6  
US-08-668-650B-14  
Sequence 14, Application US/08668650B  
Patent No. 5989920  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe P.G.  
APPLICANT: Baker, Mary W.  
APPLICANT: Branchek, Theresa  
APPLICANT: Welinschank, Richard L.  
TITLE OF INVENTION: Methods of Modifying Feeding Behavior,  
TITLE OF INVENTION: Compounds useful in such Methods, and DNA Encoding a  
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide Y Receptor  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668,650B  
FILING DATE: 04-JUN-1996  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/46166C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 456 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-668-650B-14

Query Match 88.0%; Score 1616.5; DB 2; Length 456;  
Best Local Similarity 71.6%; Pred. No. 2.4e-130;  
Matches 326; Conservative 8; Mismatches 16; Indels 105; Gaps 3;

QY 1 MSFYSKODYNNDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOQYFLIGLYTF 60  
DB 1 MSFYSKODYNNDELDEYYNKTATENTNTAATRNSDPFVMDYKSSVDDLOQYFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALMKRRKQKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLDQMMFG 120  
DB 61 VSLGFMGNLLILMALMKRRKQKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLDQMMFG 120  
QY 121 KVMCHIMFLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLIATVWTGFAI 180  
DB 121 KVMCHIMFLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLIATVWTGFAI 180  
QY 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240  
DB 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240  
QY 241 HTSVC-----IRLKR----- 251  
DB 241 HTSVCRTISGSLSNKENLEENEMINTLPFKSKGPQVKLSSHKMSYSFIKKRRRYS 300  
QY 252 -----NNMMDKM 258  
DB 301 KKTACVLPAPARPOENHSRLPENFGSVRSQSSSKFTIGVPTCFEIKPENSDVHDM 360  
QY 259 RDNK---YRSRSRSVEYRLTILILVFAVSWMPHLHFVVTDFDNDLISNRHFKLVYCIC 315  
DB 361 RVKRSVTRIKRKSRSVYRLTILILVFAVSWMPHLHFVVTDFDNDLISNRHFKLVYCIC 420  
QY 316 HLLGMSCCLNPILYGFNLNGIKADLVSLIQLCHM 350  
DB 421 HLLGMSCCLNPILYGFNLNGIKADLVSLIQLCHM 455

RESULT 7  
US-08-630-118A-6  
Sequence 6, Application US/08630118A  
Patent No. 5919901  
GENERAL INFORMATION:  
APPLICANT: Hu Ph.D., Yinghe  
APPLICANT: McCalieb Ph.D., Michael L.  
APPLICANT: Bloomquist Ph.D., Brian T.  
APPLICANT: Flores-Riveros Ph.D., Jaime R.  
APPLICANT: Cornfield Ph.D., Linda J.  
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
TITLE OF INVENTION: Sequences  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,118A
; FILING DATE: April 8, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-118A-6
```

```

Query Match      87.9%; Score 1613.5; DB 2; Length 445;
Best Local Similarity 72.6%; Pred. No. 4,2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
```

```

QY 11 MDLELDYKTKTLATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFGNLT 70
D 1 MDLELDYKTKTLATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFGNLT 60
QY 71 LILMALKKRNQKTTVFLIGNLAFSDILVVLFCSPPTLTSVLLDDMMFGKVMCHIMFPL 130
D 61 LILMALKKRNQKTTVFLIGNLAFSDILVVLFCSPPTLTSVLLDDMMFGKVMCHIMFPL 120
QY 131 QCVSVLSTLILSLIAIVRYHMIKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 190
D 121 QCVSVLSTLILSLIAIVRYHMIKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 180
QY 191 VELQETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTSHTSVC-----I 246
D 181 VELQETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTSHTSVC-----I 240
QY 247 RLKRRNNMMK-----S 257
D 241 GLSKNEKRLLENEMINTLHPSSKSGPOVKLSGSHKWSYFIKKHRRRSKKTACVLPAP 300
QY 258 ---MRDNKYY-----S 265
D 301 ERPSQENHSRLPENFGSVASQSSSKFTPGVPTCEIKPEENSDVHELKRVKRSVTRIK 360
QY 266 SRSRSVYRLLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLVYCIHLLGMSSCCL 325
D 361 KRSRSVYRLLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLVYCIHLLGMSSCCL 420
QY 326 NPILYGLNNGIKADVSLIHCLHM 350
D 421 NPILYGLNNGIKADVSLIHCLHM 445
```

```

RESULT 8
US-08-838-399-6
; Sequence 6, Application US/08838399
; Patent No. 5965392
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: Mccaleb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; TITLE OF INVENTION: Sequences
; NUMBER OF SEQUENCES: 8
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-399-6
```

```

Query Match      87.9%; Score 1613.5; DB 2; Length 445;
Best Local Similarity 72.6%; Pred. No. 4,2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
```

```

QY 11 MDLELDYKTKTLATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFGNLT 70
D 1 MDLELDYKTKTLATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFGNLT 60
QY 71 LILMALKKRNQKTTVFLIGNLAFSDILVVLFCSPPTLTSVLLDDMMFGKVMCHIMFPL 130
D 61 LILMALKKRNQKTTVFLIGNLAFSDILVVLFCSPPTLTSVLLDDMMFGKVMCHIMFPL 120
QY 131 QCVSVLSTLILSLIAIVRYHMIKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 190
D 121 QCVSVLSTLILSLIAIVRYHMIKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 180
QY 191 VELQETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTSHTSVC-----I 246
D 181 VELQETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTSHTSVC-----I 240
QY 247 RLKRRNNMMK-----S 257
D 241 GLSKNEKRLLENEMINTLHPSSKSGPOVKLSGSHKWSYFIKKHRRRSKKTACVLPAP 300
QY 258 ---MRDNKYY-----S 265
D 301 ERPSQENHSRLPENFGSVASQSSSKFTPGVPTCEIKPEENSDVHELKRVKRSVTRIK 360
QY 266 SRSRSVYRLLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLVYCIHLLGMSSCCL 325
D 361 KRSRSVYRLLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLVYCIHLLGMSSCCL 420
QY 326 NPILYGLNNGIKADVSLIHCLHM 350
D 421 NPILYGLNNGIKADVSLIHCLHM 445
```

```

RESULT 9
US-09-003-199-21
; Sequence 21, Application US/09003199
; Patent No. 5985616
; GENERAL INFORMATION:
```

APPLICANT: Parker, Eric M  
APPLICANT: Strader, Catherine D  
APPLICANT: Rudinski, Mark S  
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: NJ  
COUNTRY: USA  
ZIP: 07033-0530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.5.3  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,199  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Thampoe, Immac J  
REGISTRATION NUMBER: 36,322  
REFERENCE/DOCKET NUMBER: CN0775  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)298-5061  
TELEFAX: (908)298-5388  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-199-21

Query Match 87.9%; Score 1613.5; DB 2; Length 445;  
Best Local Similarity 72.6%; Pred. No. 4.2e-130;  
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 11 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 70  
DB 1 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 60  
QY 71 LILMALMKRRNQKTTVNFLLGNLAFSDILVLFCSPTLTSLVLDQMMFGKVMCHIMFPL 130  
DB 61 LILMALMKRRNQKTTVNFLLGNLAFSDILVLFCSPTLTSLVLDQMMFGKVMCHIMFPL 120  
QY 131 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFAICSPLPVPHSL 190  
DB 121 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFAICSPLPVPHSL 180  
QY 191 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVC---I 246  
DB 181 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 240  
QY 247 RLKRRNNMMDK----- 257  
DB 241 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKMSYFIKKHRRRYSKTACVLPAP 300  
QY 258 ---MRDKYR-----S 265  
DB 301 ERPSQENHSRIPLPNFGSVRSQSSSKFLPGVPTCFEIKPEENSDVHELKRVKSVTRIK 360  
QY 266 SRSQSVYRLITLLVFAVSMPLHFLVYVTDENDNLISNHEKLYVCICHLGMMSCCL 325  
DB 361 KRSSSVYRLITLLVFAVSMPLHFLVYVTDENDNLISNHEKLYVCICHLGMMSCCL 420  
QY 326 NPILYGLNNGIKADLVSLIHCLHM 350  
DB 421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 10  
US-09-235-839-6  
Sequence 6, Application US/09235839  
Patent No. 6207799  
GENERAL INFORMATION:  
APPLICANT: Hu Ph.D., Yinghe  
APPLICANT: McCalcd Ph.D., Michael L.  
APPLICANT: Bloomquist Ph.D., Brian T.  
APPLICANT: Flores-Riveros Ph.D., Jaime R.  
APPLICANT: Cornfield Ph.D., Linda J.  
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/235,839  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,118  
FILING DATE: April 8, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenfield Ph.D., Michael S.  
REGISTRATION NUMBER: 37,142  
REFERENCE/DOCKET NUMBER: 96,149-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)913-0001  
TELEFAX: (312)913-0002  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-235-839-6

Query Match 87.9%; Score 1613.5; DB 4; Length 445;  
Best Local Similarity 72.6%; Pred. No. 4.2e-130;  
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;  
QY 11 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 70  
DB 1 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 60  
QY 71 LILMALMKRRNQKTTVNFLLGNLAFSDILVLFCSPTLTSLVLDQMMFGKVMCHIMFPL 130  
DB 61 LILMALMKRRNQKTTVNFLLGNLAFSDILVLFCSPTLTSLVLDQMMFGKVMCHIMFPL 120  
QY 131 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFAICSPLPVPHSL 190  
DB 121 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFAICSPLPVPHSL 180  
QY 191 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVC---I 246  
DB 181 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 240  
QY 247 RLKRRNNMMDK----- 257  
DB 241 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKMSYFIKKHRRRYSKTACVLPAP 300  
QY 258 ---MRDKYR-----S 265

Db 301 ERPSQEHSHILPENGSVRSQSSSKFTPGVPTCEIKPEENSDVHELVRKSVTRIK 360  
QY 266 SRSRSVFRLLTILILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCICHLGMMSCCL 325  
|||||  
Db 361 KRSRSVFRLLTILILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCICHLGMMSCCL 420  
QY 326 NPILYGFLLNGIKADLVSLIHCLHM 350  
|||||  
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

RESULT 11  
US-09-327-035-6  
; Sequence 6, Application US/09327035  
; Patent No. 6368824  
; GENERAL INFORMATION:  
; APPLICANT: Hu Ph.D., Yinghe  
; McCaleb Ph.D., Michael L.  
; Bloomquist Ph.D., Brian T.  
; Flores-Riveros Ph.D., Jaime R.  
; Cornfield Ph.D., Linda J.  
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
; Sequences  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/327,035  
; FILING DATE: 07-Jun-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/838,399  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greenfield Ph.D., Michael S.  
; REGISTRATION NUMBER: 37,147  
; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)715-1000  
; TELEFAX: (312)715-1234  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-327-035-6

Query Match 87.9%; Score 1613.5; DB 4; Length 445;  
Best Local Similarity 72.6%; Pred. No. 4.2e-130;  
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 11 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDLDQYFLIGLYTFVSLGFMGNL 70  
|||||  
Db 1 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDLDQYFLIGLYTFVSLGFMGNL 60  
QY 71 LILMALMKRRNOKTYVNFILGNLAFSDDILVLFCSPTLTSVLLDDQMGKVMCHIMPEL 130  
|||||  
Db 61 LILMALMKRRNOKTYVNFILGNLAFSDDILVLFCSPTLTSVLLDDQMGKVMCHIMPEL 120  
QY 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFFLIATYWTIGFAICSPLPVPHSL 190  
|||||

Db 121 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFFLIATYWTIGFAICSPLPVPHSL 180  
QY 191 VELQETFGSALLSSRYLCVSWPSSDYRIAFITSLILVQYILPLVCLTVSHTSVC----I 246  
|||||  
Db 181 VELQETFGSALLSSRYLCVSWPSSDYRIAFITSLILVQYILPLVCLTVSHTSVCISISC 240  
QY 247 RLKRRNNMMDK----- 257  
| : | : :  
Db 241 GLSNKENRLEENEMINLTLHPSKSGPQVXLGSHKWSYFIKKHRRRYSKTACVLPAP 300  
QY 258 ---MROKVR-----S 265  
| : | : |  
Db 301 ERPSQEHSHILPENGSVRSQSSSKFTPGVPTCEIKPEENSDVHELVRKSVTRIK 360  
QY 266 SRSRSVFRLLTILILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCICHLGMMSCCL 325  
|||||  
Db 361 KRSRSVFRLLTILILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCICHLGMMSCCL 420  
QY 326 NPILYGFLLNGIKADLVSLIHCLHM 350  
|||||  
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

RESULT 12  
US-09-040-958-2  
; Sequence 2, Application US/09040958  
; Patent No. 6242251  
; GENERAL INFORMATION:  
; APPLICANT: Baez, Melvyn  
; TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y5 RECEPTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/040,958  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-11350  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-040-958-2

Query Match 87.7%; Score 1610.5; DB 4; Length 445;  
Best Local Similarity 72.4%; Pred. No. 7.5e-130;  
Matches 322; Conservative 7; Mismatches 11; Indels 105; Gaps 3;

QY 11 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDLDQYFLIGLYTFVSLGFMGNL 70  
|||||  
Db 1 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDLDQYFLIGLYTFVSLGFMGNL 60  
QY 71 LILMALMKRRNOKTYVNFILGNLAFSDDILVLFCSPTLTSVLLDDQMGKVMCHIMPEL 130  
|||||  
Db 61 LILMALMKRRNOKTYVNFILGNLAFSDDILVLFCSPTLTSVLLDDQMGKVMCHIMPEL 120

```

QY 131 QCVSVLSTLLISIALVRHMKIKHRISNNLTANHGVELLATWTTGALCSLPVPHSL 190
Db 121 QCVSVLSTLLISIALVRHMKIKHRISNNLTANHGVELLATWTTGALCSLPVPHSL 180
QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFETISLLVOYITLPLVCLTGHSTGVC---I 246
Db 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFETISLLVOYITLPLVCLTGHSTGVCISG 240
QY 247 RLKRRNNMMDK-----257
Db 241 GLSKREKRELEENEMINLTLPKRKIGPQVKLSGHHKMSYSFIKKHRRRYSKTACVLPAP 300
QY 258 ---NRDKKYY-----S 265
Db 301 ERPSQEHNRSLIPENFGSVRSQSSSKFTPGVTCPEIRPENSVDVHLLRVKRSYTRIK 360
QY 266 SRSSSVYRRLIILVLAVASMPRLHLEFHYVTDPRNDLISRNHKKLYCICHLIGMSSCL 325
Db 361 KRSSSVYRRLIILVLAVASMPRLHLEFHYVTDPRNDLISRNHKKLYCICHLIGMSSCL 420
QY 326 NPILYGLNNGIKADVLSTLHCLHM 350
Db 421 NPILYGLNNGIKADVLSTLHCLHM 445

```

```

RESULT 13
US-09-040-958-4
; Sequence 4, Application US/09040958
; Patent No. 6242251
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y5 RECEPTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040_958
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-11350
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-09-040-958-4

```

Query Match	Best Local Match	Similarity	Score	Length	DB
Matches 322;	Conservative	72.4%	1610.5	445;	DB 4;
			Pred. No. 7.5-130;		
			Mismatches 11;	Indels 105;	Gaps 3;

QY	71	LIILAIKKRRKQKTTVFELIGNLAFSDILVLFCSPTLTVSYLLDDMPCKWCHIMFPL	130
Db	61	LILAIKKRRKQKTTVFELIGNLAFSDILVLFCSPTLTVSYLLDDMPCKWCHIMFPL	120
QY	131	QCVSVLSTLLISIAIVRYHMIKPIISNNLTANHGYELIATWTLGFAICSPLPVFHSL	190
Db	121	QCVSVLSTLLISIAIVRYHMIKPIISNNLTANHGYELIATWTLGFAICSPLPVFHSL	180
QY	191	VELDFTGSAIISSRYLCVESWPSDSRIAFITISLLVQYILPLVCLTVSHSTVC---	246
Db	181	VELDFTGSAIISSRYLCVESWPSDSRIAFITISLLVQYILPLVCLTVSHSTVCRSISC	240
QY	247	RLKRRNNMMDK-----	257
Db	241	GLSKENKPLENEMINILTLHPSKIGPQVAKLGSCHKWYSYFIKKHRRYSKKTACVLPAP	300
QY	258	---WRDKKYR-----S	265
Db	301	ERPSQENHSRIPLPENFGSVSLSQSSSKFIIPGVPTCEIKREPSNDVHELRYKRSVTRIK	360
QY	266	SRSRSVFYRLTILILVAVSWMPDLHFVVTVDENDNISNRHFKLYVCICHLIGMSSCCL	325
Db	361	KRSRSVFYRLTILILVAVSWMPDLHFVVTVDENDNISNRHFKLYVCICHLIGMSSCCL	420
QY	326	NPILYGFLLNGIKADVLSLHCLHM	350
Db	421	NPILYGFLLNGIKADVLSLHCLHM	445

```

RESULT 14
US-09-003-199-2
: Sequence 2, Application US/09003199
: Patent No. 5985616
: GENERAL INFORMATION:
: APPLICANT: Parker, Eric M
: APPLICANT: Strader, Catherine D
: APPLICANT: Rudinski, Mark S
: TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schering-Plough Corporation
: STREET: 2000 Galloping Hill Road
: CITY: Kenilworth
: STATE: NJ
: COUNTRY: USA
: ZIP: 07033-0530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 7.5.3
: SOFTWARE: Microsoft Word 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/003.199
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Thampoe, Immac J
: REGISTRATION NUMBER: 36,322
: REFERENCE/DOCKET NUMBER: CN0775
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908)298-5061
: TELEFAX: (908)298-5388
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 445 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IS-09-003-199-2

```

Query Match	84.4%;	Score 1549.5;	DB 2;	Length 445;
Best Local Similarity	69.2%;	Pred. No. 1.2e-12;		
Matches 308; Conservative	14;	Mismatches 18;	Indels 105;	Gaps 3;





**This Page Blank (uspto)**